OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 07:57:03 ; Search time 0.001 Seconds
(without alignments)
58.120 Million cell updates/sec

Title: us-09-774-809-31
Perfect score: 20
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 125 seqs, 1453 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 171 summaries

Database : rge.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	AR110470	ACCESSION:AR110470
	2	20	100.0	20	1	AR116450	ACCESSION:AR116450
c	3	20	100.0	20	1	AR116461	ACCESSION:AR116461
	4	20	100.0	20	1	AX104119	ACCESSION:AX104119
	5	20	100.0	20	1	AX164692	ACCESSION:AX164692
	6	20	100.0	20	1	AX355435	ACCESSION:AX355435
	7	20	100.0	20	1	AX547172	ACCESSION:AX547172
	8	20	100.0	20	1	BD074607	ACCESSION:BD074607
c	9	20	100.0	20	1	BD074618	ACCESSION:BD074618
c	10	15	75.0	19	1	AX129247	ACCESSION:AX129247
c	11	14.8	74.0	18	1	AR190756	ACCESSION:AR190756
c	12	14.4	72.0	17	1	AR188734	ACCESSION:AR188734
c	13	14	70.0	17	1	AR192173	ACCESSION:AR192173
	14	13.4	67.0	17	1	AR145684	ACCESSION:AR145684
	15	13.4	67.0	17	1	AR174508	ACCESSION:AR174508
c	16	13.4	67.0	17	1	AR186508	ACCESSION:AR186508
c	17	13	65.0	17	1	AR192172	ACCESSION:AR192172
c	18	12.8	64.0	17	1	AR190307	ACCESSION:AR190307
	19	10.4	52.0	12	1	AR167736	ACCESSION:AR167736
	20	10.4	52.0	12	1	E29620	ACCESSION:E29620
	21	10.4	52.0	12	1	E38726	ACCESSION:E38726
	22	10.4	52.0	12	1	E64152	ACCESSION:E64152
c	23	10	50.0	10	1	AX153495	ACCESSION:AX153495
c	24	10	50.0	10	1	AX153496	ACCESSION:AX153496
c	25	9.8	49.0	13	1	AR136587	ACCESSION:AR136587
	26	9.8	49.0	13	1	AR285088	ACCESSION:AR285088
c	27	9.8	49.0	13	1	AR285113	ACCESSION:AR285113
	28	9.8	49.0	13	1	BD091222	ACCESSION:BD091222
	29	9.4	47.0	11	1	AR301743	ACCESSION:AR301743
c	30	9.4	47.0	11	1	AX623125	ACCESSION:AX623125
c	31	9.4	47.0	11	1	AX627385	ACCESSION:AX627385
c	32	9.4	47.0	11	1	AX630546	ACCESSION:AX630546
	33	9.4	47.0	11	1	BD124493	ACCESSION:BD124493
c	34	9	45.0	11	1	AX482038	ACCESSION:AX482038
c	35	9	45.0	11	1	AX511277	ACCESSION:AX511277
c	36	9	45.0	11	1	AX623635	ACCESSION:AX623635
c	37	9	45.0	11	1	AX625164	ACCESSION:AX625164
c	38	9	45.0	11	1	AX625382	ACCESSION:AX625382
c	39	9	45.0	11	1	AX629145	ACCESSION:AX629145
c	40	9	45.0	11	1	AX629339	ACCESSION:AX629339
c	41	9	45.0	11	1	AX631056	ACCESSION:AX631056
c	42	9	45.0	11	1	AX632585	ACCESSION:AX632585
c	43	8.4	42.0	10	1	AR107817	ACCESSION:AR107817
c	44	8.4	42.0	10	1	AX152505	ACCESSION:AX152505
c	45	8.4	42.0	10	1	AX152506	ACCESSION:AX152506
	46	8.4	42.0	10	1	AX152507	ACCESSION:AX152507
	47	8.4	42.0	10	1	AX152729	ACCESSION:AX152729
c	48	8.4	42.0	10	1	AX153313	ACCESSION:AX153313
c	49	8.4	42.0	10	1	AX153314	ACCESSION:AX153314
c	50	8.4	42.0	10	1	AX153315	ACCESSION:AX153315
c	51	8.4	42.0	10	1	AX153316	ACCESSION:AX153316
c	52	8.4	42.0	10	1	AX153317	ACCESSION:AX153317
c	53	8.4	42.0	10	1	AX153318	ACCESSION:AX153318
c	54	8.4	42.0	10	1	AX153319	ACCESSION:AX153319
c	55	8.4	42.0	10	1	AX224404	ACCESSION:AX224404
	56	8.4	42.0	10	1	AX224407	ACCESSION:AX224407
c	57	8.4	42.0	10	1	AX224410	ACCESSION:AX224410
c	58	8.4	42.0	10	1	AX301480	ACCESSION:AX301480
c	59	8.4	42.0	10	1	BD007979	ACCESSION:BD007979
c	60	8.4	42.0	10	1	BD065145	ACCESSION:BD065145
c	61	8.4	42.0	10	1	BD083124	ACCESSION:BD083124
c	62	8.4	42.0	10	1	BD161262	ACCESSION:BD161262
	63	8.4	42.0	10	1	BD166487	ACCESSION:BD166487
c	64	8.4	42.0	10	1	BD166906	ACCESSION:BD166906
c	65	8.4	42.0	10	1	BD167212	ACCESSION:BD167212
c	66	8.4	42.0	10	1	E39489	ACCESSION:E39489
c	67	8.4	42.0	10	1	E39743	ACCESSION:E39743
c	68	8.4	42.0	10	1	E54829	ACCESSION:E54829
	69	8.4	42.0	11	1	AX623125	ACCESSION:AX623125
	70	8.4	42.0	11	1	AX630546	ACCESSION:AX630546
	71	8.4	42.0	11	1	AX393189	ACCESSION:AX393189
	72	8.4	42.0	11	1	AX470637	ACCESSION:AX470637
c	73	8.4	42.0	11	1	AX470751	ACCESSION:AX470751
	74	8.4	42.0	11	1	AX471339	ACCESSION:AX471339
	75	8.4	42.0	11	1	AX471385	ACCESSION:AX471385
	76	8.4	42.0	11	1	AX482027	ACCESSION:AX482027
	77	8.4	42.0	11	1	AX511266	ACCESSION:AX511266
c	78	8.4	42.0	11	1	AX623296	ACCESSION:AX623296
	79	8.4	42.0	11	1	AX623449	ACCESSION:AX623449
	80	8.4	42.0	11	1	AX623782	ACCESSION:AX623782
	81	8.4	42.0	11	1	AX625842	ACCESSION:AX625842
	82	8.4	42.0	11	1	AX625891	ACCESSION:AX625891
c	83	8.4	42.0	11	1	AX626383	ACCESSION:AX626383
	84	8.4	42.0	11	1	AX626723	ACCESSION:AX626723
c	85	8.4	42.0	11	1	AX626887	ACCESSION:AX626887
c	86	8.4	42.0	11	1	AX627709	ACCESSION:AX627709
c	87	8.4	42.0	11	1	AX628172	ACCESSION:AX628172
	88	8.4	42.0	11	1	AX628292	ACCESSION:AX628292
c	89	8.4	42.0	11	1	AX629263	ACCESSION:AX629263
c	90	8.4	42.0	11	1	AX629507	ACCESSION:AX629507
	91	8.4	42.0	11	1	AX629798	ACCESSION:AX629798
c	92	8.4	42.0	11	1	AX629883	ACCESSION:AX629883
c	93	8.4	42.0	11	1	AX630156	ACCESSION:AX630156
c	94	8.4	42.0	11	1	AX630273	ACCESSION:AX630273
c	95	8.4	42.0	11	1	AX630717	ACCESSION:AX630717
	96	8.4	42.0	11	1	AX630870	ACCESSION:AX630870
	97	8.4	42.0	11	1	AX631203	ACCESSION:AX631203
c	98	8.4	42.0	11	1	BD135851	ACCESSION:BD135851
c	99	8	40.0	9	1	A94680	ACCESSION:A94680
c	100	8	40.0	9	1	AX023498	ACCESSION:AX023498
c	101	8	40.0	9	1	AX668925	ACCESSION:AX668925
c	102	8	40.0	9	1	AX668927	ACCESSION:AX668927
c	103	8	40.0	9	1	AX668975	ACCESSION:AX668975
	104	8	40.0	10	1	AX153313	ACCESSION:AX153313
	105	8	40.0	10	1	AX153314	ACCESSION:AX153314
	106	8	40.0	10	1	AX153315	ACCESSION:AX153315

107	8	40.0	10	1	AX153316	ACCESSION:AX153316
108	8	40.0	10	1	AX153317	ACCESSION:AX153317
109	8	40.0	10	1	AX153318	ACCESSION:AX153318
110	8	40.0	10	1	AX153319	ACCESSION:AX153319
111	8	40.0	10	1	BD083124	ACCESSION:BD083124
112	8	40.0	10	1	BD161262	ACCESSION:BD161262
113	8	40.0	10	1	BD167212	ACCESSION:BD167212
114	8	40.0	10	1	E39489	ACCESSION:E39489
115	8	40.0	10	1	E54829	ACCESSION:E54829
c 116	8	40.0	10	1	AR058606	ACCESSION:AR058606
c 117	8	40.0	10	1	AR088590	ACCESSION:AR088590
118	8	40.0	10	1	AX152706	ACCESSION:AX152706
c 119	8	40.0	10	1	AX152961	ACCESSION:AX152961
c 120	8	40.0	10	1	AX152962	ACCESSION:AX152962
c 121	8	40.0	10	1	AX153299	ACCESSION:AX153299
c 122	8	40.0	10	1	AX153300	ACCESSION:AX153300
123	8	40.0	10	1	BD007922	ACCESSION:BD007922
c 124	8	40.0	10	1	BD007953	ACCESSION:BD007953
125	8	40.0	10	1	BD083213	ACCESSION:BD083213
c 126	8	40.0	10	1	BD083308	ACCESSION:BD083308
127	8	40.0	10	1	BD161348	ACCESSION:BD161348
128	8	40.0	10	1	BD166572	ACCESSION:BD166572
129	8	40.0	10	1	BD167054	ACCESSION:BD167054
130	8	40.0	10	1	E54715	ACCESSION:E54715
131	7.8	39.0	11	1	AX482038	ACCESSION:AX482038
132	7.8	39.0	11	1	AX511277	ACCESSION:AX511277
133	7.8	39.0	11	1	AX625382	ACCESSION:AX625382
134	7.8	39.0	11	1	AX470751	ACCESSION:AX470751
135	7.8	39.0	11	1	AX629883	ACCESSION:AX629883
c 136	7.8	39.0	17	1	AR145684	ACCESSION:AR145684
c 137	7.8	39.0	17	1	AR174508	ACCESSION:AR174508
c 138	7.6	38.0	20	1	AR110470	ACCESSION:AR110470
c 139	7.6	38.0	20	1	AR116450	ACCESSION:AR116450
140	7.6	38.0	20	1	AR116461	ACCESSION:AR116461
c 141	7.6	38.0	20	1	AX104119	ACCESSION:AX104119
c 142	7.6	38.0	20	1	AX164692	ACCESSION:AX164692
c 143	7.6	38.0	20	1	AX355435	ACCESSION:AX355435
c 144	7.6	38.0	20	1	AX547172	ACCESSION:AX547172
c 145	7.6	38.0	20	1	BD074607	ACCESSION:BD074607
146	7.6	38.0	20	1	BD074618	ACCESSION:BD074618
147	7.4	37.0	9	1	AX205250	ACCESSION:AX205250
148	7.4	37.0	9	1	AX668699	ACCESSION:AX668699
149	7.4	37.0	9	1	AX668700	ACCESSION:AX668700
150	7.4	37.0	10	1	AX224404	ACCESSION:AX224404
c 151	7.4	37.0	10	1	AX224407	ACCESSION:AX224407
152	7.4	37.0	10	1	AX224410	ACCESSION:AX224410
153	7.4	37.0	10	1	AX153299	ACCESSION:AX153299
154	7.4	37.0	10	1	AX153300	ACCESSION:AX153300
155	7.4	37.0	10	1	BD007953	ACCESSION:BD007953
c 156	7.4	37.0	11	1	AX625842	ACCESSION:AX625842
157	7.4	37.0	11	1	AX630156	ACCESSION:AX630156
158	7.4	37.0	19	1	AX129247	ACCESSION:AX129247
c 159	7	35.0	9	1	AX017438	ACCESSION:AX017438
c 160	7	35.0	9	1	AX538878	ACCESSION:AX538878
c 161	7	35.0	9	1	AX668947	ACCESSION:AX668947
c 162	7	35.0	9	1	AX668948	ACCESSION:AX668948
c 163	7	35.0	9	1	BD138429	ACCESSION:BD138429
c 164	7	35.0	11	1	AX471339	ACCESSION:AX471339
c 165	7	35.0	11	1	AX623782	ACCESSION:AX623782
c 166	7	35.0	11	1	AX631203	ACCESSION:AX631203
167	6.8	34.0	10	1	AX152961	ACCESSION:AX152961
168	6.8	34.0	10	1	AX152962	ACCESSION:AX152962
169	6.8	34.0	11	1	AX629507	ACCESSION:AX629507
170	6.4	32.0	8	1	E63474	ACCESSION:E63474
c 171	6.4	32.0	8	1	E63474	ACCESSION:E63474

ALIGNMENTS

```
RESULT 1
AR110470
LOCUS       AR110470                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 7 from patent US 6114517.
ACCESSION   AR110470
VERSION     AR110470.1  GI:12826746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Xu,X.S.
  TITLE     Methods of modulating tumor necrosis factor .alpha.-induced
            expression of cell adhesion molecules
  JOURNAL   Patent: US 6114517-A 7 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 2
AR116450
LOCUS       AR116450                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6133246.
ACCESSION   AR116450
VERSION     AR116450.1  GI:14096772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 31 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 3
AR116461/c
LOCUS       AR116461                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 42 from patent US 6133246.
ACCESSION   AR116461
VERSION     AR116461.1  GI:14096783
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 42 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
```

```
BASE COUNT        2 a      7 c      7 g      4 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db         20 GTCCGGGCCAGGCCAAAGTC 1


RESULT 4
AX104119
LOCUS       AX104119                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 311 from Patent WO0122972.
ACCESSION   AX104119
VERSION     AX104119.1  GI:13920316
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 311 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 5
AX164692
LOCUS       AX164692                  20 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0134792.
ACCESSION   AX164692
VERSION     AX164692.1  GI:14545586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Potapova,O., Gorospe,M. and Holbrook,N.J.
  TITLE     Compositions and methods for the diminution or elimination of
            various cancers
  JOURNAL   Patent: WO 0134792-A 2 17-MAY-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 6
AX355435
LOCUS       AX355435                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 463 from Patent WO0197843.
ACCESSION   AX355435
VERSION     AX355435.1  GI:18620103
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 463 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~phosphorothioate
                     backbone"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 7
AX547172
LOCUS       AX547172                  20 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 311 from Patent WO02053141.
ACCESSION   AX547172
VERSION     AX547172.1  GI:25812316
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 311 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 8
BD074607
LOCUS       BD074607                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisence oligonucleotide composition and modulation method of JNK
```

```
            protein.
ACCESSION   BD074607
VERSION     BD074607.1  GI:22620210
KEYWORDS    JP 2001514905-A/31.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mckay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
  TITLE     Antisence oligonucleotide composition and modulation method of JNK
            protein
  JOURNAL   Patent: JP 2001514905-A 31 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514905-A/31
            PD   18-SEP-2001
            PF   07-AUG-1998 JP 2000509875
            PR   13-AUG-1997 US    08/910629
            PI   ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO,WILLIAM A GAARDE
            PC   C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC   C12N15/00
            CC   antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 9
BD074618/c
LOCUS       BD074618                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisence oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION   BD074618
VERSION     BD074618.1  GI:22620221
KEYWORDS    JP 2001514905-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mckay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
  TITLE     Antisence oligonucleotide composition and modulation method of JNK
            protein
  JOURNAL   Patent: JP 2001514905-A 42 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514905-A/42
            PD   18-SEP-2001
            PF   07-AUG-1998 JP 2000509875
            PR   13-AUG-1997 US    08/910629
            PI   ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO,WILLIAM A GAARDE
            PC   C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC   C12N15/00
            CC   control sequence (sense)
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        2 a      7 c      7 g      4 t

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db         20 GTCCGGGCCAGGCCAAAGTC 1


RESULT 10
AX129247/c
LOCUS       AX129247                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 465 from Patent WO0130362.
ACCESSION   AX129247
VERSION     AX129247.1  GI:14135552
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 465 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /note="Cdk4 ribozyme binding site"
BASE COUNT        1 a      6 c      7 g      5 t

  Query Match             75.0%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              |||||||||||||||
Db         19 GGCCAGGCCAAAGTC 5


RESULT 11
AR190756/c
LOCUS       AR190756                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6244 from patent US 6346398.
ACCESSION   AR190756
VERSION     AR190756.1  GI:20236721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 6244 12-FEB-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
BASE COUNT        1 a      6 c      7 g      4 t

  Query Match             74.0%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3.1;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          3 CCGGGCCAGGCCAAAGTC 20
              |||||||| ||| |||||
Db         18 CCGGGCCAAGCCGAAGTC 1


RESULT 12
AR188734/c
LOCUS       AR188734                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4222 from patent US 6346398.
ACCESSION   AR188734
VERSION     AR188734.1  GI:20234699
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 4222 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      5 c      7 g      5 t

  Query Match            72.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity  93.8%;  Pred. No. 3.6;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              |||||||| |||||||
Db         16 CCGGGCCAAGCCAAAG 1


RESULT 13
AR192173/c
LOCUS       AR192173                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7661 from patent US 6346398.
ACCESSION   AR192173
VERSION     AR192173.1  GI:20238138
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7661 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      5 c      6 g      5 t

  Query Match            70.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 4.5;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAAAGTC 20
              ||||||||||||||
Db         17 GCCAGGCCAAAGTC 4


RESULT 14
AR145684
LOCUS       AR145684                  17 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6218109.
ACCESSION   AR145684
VERSION     AR145684.1  GI:15108873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Elledge,S.J. and Sanchez,Y.
  TITLE     Mammalian checkpoint genes and proteins
  JOURNAL   Patent: US 6218109-A 6 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      4 c      5 g      3 t

  Query Match            67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity  93.3%;  Pred. No. 6.5;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              || ||||||||||||
Db          3 GGACAGGCCAAAGTC 17


RESULT 15
AR174508
LOCUS       AR174508                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 6 from patent US 6307015.
ACCESSION   AR174508
VERSION     AR174508.1  GI:17914828
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Elledge,S.J. and Sanchez,Y.
  TITLE     Mammalian checkpoint genes and proteins
  JOURNAL   Patent: US 6307015-A 6 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      4 c      5 g      3 t

  Query Match            67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity  93.3%;  Pred. No. 6.5;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              || ||||||||||||
Db          3 GGACAGGCCAAAGTC 17


RESULT 16
AR186508/c
LOCUS       AR186508                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1996 from patent US 6346398.
ACCESSION   AR186508
VERSION     AR186508.1  GI:20232473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 1996 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      5 c      6 g      5 t

  Query Match            67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity  93.3%;  Pred. No. 6.5;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAA 17
              ||||||| ||||||||
Db         15 CCGGGCAAGGCCAAA 1
```

```
RESULT 17
AR192172/c
LOCUS       AR192172                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7660 from patent US 6346398.
ACCESSION   AR192172
VERSION     AR192172.1  GI:20238137
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7660 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      4 c      6 g      6 t

  Query Match             65.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.3;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAAGTC 20
              |||||||||||||
Db         17 CCAGGCCAAAGTC 5


RESULT 18
AR190307/c
LOCUS       AR190307                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 5795 from patent US 6346398.
ACCESSION   AR190307
VERSION     AR190307.1  GI:20236272
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 5795 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      6 c      7 g      4 t

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 9.3;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              |||||||| ||| |||
Db         16 CCGGGCCAAGCCGAAG 1


RESULT 19
AR167736
LOCUS       AR167736                  12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 100 from patent US 6287769.
ACCESSION   AR167736
VERSION     AR167736.1  GI:17903536
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,T.
  TITLE     Method of amplifying DNA fragment, apparatus for amplifying DNA
            fragment, method of assaying microorganisms, method of analyzing
            microorganisms and method of assaying contaminant
  JOURNAL   Patent: US 6287769-A 100 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
BASE COUNT        3 a      4 c      4 g      1 t

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 22;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 20
E29620
LOCUS       E29620                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste.
ACCESSION   E29620
VERSION     E29620.1  GI:13021123
KEYWORDS    JP 1999276176-A/100.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste
  JOURNAL   Patent: JP 1999276176-A 100 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 1999276176-A/100
            PD   12-OCT-1999
            PF   31-MAR-1998 JP 1998087652
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
            Strandedness: Single;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      4 g      1 t

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 22;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 21
E38726
LOCUS       E38726                    12 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method and device for amplifying DNA fragment.
ACCESSION   E38726
VERSION     E38726.1  GI:18621388
KEYWORDS    JP 2000270867-A/100.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
```

```
  AUTHORS   Inoue,K.
  TITLE     Method and device for amplifying DNA fragment
  JOURNAL   Patent: JP 2000270867-A 100 03-OCT-2000;
            SANYO ELECTRIC CO.LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 2000270867-A/100
            PD   03-OCT-2000
            PF   19-MAR-1999 JP 1999076844
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      4 g      1 t

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 22;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 22
E64152
LOCUS       E64152                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, amplification apparatus of DNA
             fragment, method for assaying a group of microorganisms, method
            for analyzing a group of microorganisms, and method for assaying
            contaminating  substance.
ACCESSION   E64152
VERSION     E64152.1  GI:13019556
KEYWORDS    JP 1999341989-A/100.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method for
            analyzing a group of microorganisms, and method for assaying
            contaminating substance
  JOURNAL   Patent: JP 1999341989-A 100 14-DEC-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Artificial Sequence
            PN   JP 1999341989-A/100
            PD   14-DEC-1999
            PF   16-MAR-1999 JP 1999069694
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      4 c      4 g      1 t

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 22;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 23
AX153495/c
LOCUS       AX153495                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1410 from Patent WO0138577.
ACCESSION   AX153495
VERSION     AX153495.1  GI:14535146
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1410 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||||||||||
Db         10 TCCGGGCCAG 1


RESULT 24
AX153496/c
LOCUS       AX153496                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1411 from Patent WO0138577.
ACCESSION   AX153496
VERSION     AX153496.1  GI:14535147
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1411 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||||||||||
Db         10 TCCGGGCCAG 1
```

```
RESULT 25
AR136587/c
LOCUS       AR136587                  13 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 77 from patent US 6136952.
ACCESSION   AR136587
VERSION     AR136587.1  GI:14477259
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Li,L. and Hood,L.
  TITLE     Human jagged polypeptide, encoding nucleic acids and methods of use
  JOURNAL   Patent: US 6136952-A 77 24-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
BASE COUNT        0 a      4 c      6 g      3 t

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 35;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCCAAA 17
              |||||| |||| |
Db         13 GGGCCACGCCACA 1


RESULT 26
AR285088
LOCUS       AR285088                  13 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 11 from patent US 6528268.
ACCESSION   AR285088
VERSION     AR285088.1  GI:29722005
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Andersson,M.K., Berglund,L.G.T., Reneland,R.H. and Adam,G.I.R.
  TITLE     Reagents and methods for detection of heart failure
  JOURNAL   Patent: US 6528268-A 11 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
BASE COUNT        3 a      7 c      3 g      0 t

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 35;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCA 15
              |||  ||||||||
Db          1 CCGACCCAGGCCA 13


RESULT 27
AR285113/c
LOCUS       AR285113                  13 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 36 from patent US 6528268.
ACCESSION   AR285113
VERSION     AR285113.1  GI:29722030
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Andersson,M.K., Berglund,L.G.T., Reneland,R.H. and Adam,G.I.R.
  TITLE     Reagents and methods for detection of heart failure
  JOURNAL   Patent: US 6528268-A 36 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
BASE COUNT        0 a      3 c      7 g      3 t

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 35;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCA 15
              |||  ||||||||
Db         13 CCGACCCAGGCCA 1


RESULT 28
BD091222
LOCUS       BD091222                  13 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Hetero dimer fused proteins useful against targeting immunotherapy
            and general immunostimulation.
ACCESSION   BD091222
VERSION     BD091222.1  GI:22636832
KEYWORDS    JP 2001525423-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Gillies,S.D., Lo,K.M. and Lan,Y.
  TITLE     Hetero dimer fused proteins useful against targeting immunotherapy
            and general immunostimulation
  JOURNAL   Patent: JP 2001525423-A 7 11-DEC-2001;
            LEXIGEN PHARMACEUTICALS CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2001525423-A/7
            PD   11-DEC-2001
            PF   08-DEC-1998 JP 2000524321
            PR   08-DEC-1997 US    08/986997
            PI   STEPHEN D GILLIES,KIN MING LO,YAN LAN
            PC   C07K19/00,A61K47/48,A61P37/04,C07K14/54,C07K16/30,C12N15/09,
            PC   C12P21/00//
            PC   A61K38/00,C12N15/00,A61K37/02
            CC   Description of Artificial Sequence: Synthetic Oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .13
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      5 c      4 g      1 t

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 35;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCA 15
              ||||||  || |||
Db          1 CCGGGCAAGTCCA 13


RESULT 29
AR301743
LOCUS       AR301743                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 324 from patent US 6538173.
ACCESSION   AR301743
VERSION     AR301743.1  GI:31689545
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 324 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .11
```

```
                     /organism="unknown"
BASE COUNT        1 a      3 c      6 g      1 t

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAGG 12
              ||||||| |||
Db          1 TCCGGGCGAGG 11


RESULT 30
AX623125/c
LOCUS       AX623125                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 166 from Patent WO02053774.
ACCESSION   AX623125
VERSION     AX623125.1  GI:28451066
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 166 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      5 g      1 t

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              || ||||||||
Db         11 CCTGGCCAGGC 1


RESULT 31
AX627385/c
LOCUS       AX627385                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4426 from Patent WO02053774.
ACCESSION   AX627385
VERSION     AX627385.1  GI:28455423
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4426 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      2 c      4 g      5 t

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAAA 17
              |||| ||||||
Db         11 GCCAAGCCAAA 1


RESULT 32
AX630546/c
LOCUS       AX630546                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7587 from Patent WO02053774.
ACCESSION   AX630546
VERSION     AX630546.1  GI:28458584
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7587 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      5 g      1 t

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              || ||||||||
Db         11 CCTGGCCAGGC 1


RESULT 33
BD124493
LOCUS       BD124493                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124493
VERSION     BD124493.1  GI:23219438
KEYWORDS    JP 2002503460-A/324.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 324 05-FEB-2002;
            THE WISTAR INSTITUTE
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/324
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        1 a      3 c      6 g      1 t

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 33;
```

```
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAGG 12
              ||||||| |||
Db          1 TCCGGGCGAGG 11


RESULT 34
AX482038/c
LOCUS       AX482038                 11 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 15 from Patent EP1225233.
ACCESSION   AX482038
VERSION     AX482038.1  GI:22316760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1225233-A 15 24-JUL-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TAG sequence Hs74649 and Hs288761"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||||||||
Db         11 GGCCAGGCC 3


RESULT 35
AX511277/c
LOCUS       AX511277                 11 bp    DNA     linear   PAT 28-SEP-2002
DEFINITION  Sequence 15 from Patent WO02059558.
ACCESSION   AX511277
VERSION     AX511277.1  GI:23392154
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: WO 02059558-A 15 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TAG sequence Hs74649 and Hs288761"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||||||||
Db         11 GGCCAGGCC 3


RESULT 36
AX623635/c
LOCUS       AX623635                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 676 from Patent WO02053774.
ACCESSION   AX623635
VERSION     AX623635.1  GI:28451576
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 676 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      2 c      3 g      5 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAA 17
              |||||||||
Db         10 CAGGCCAAA 2


RESULT 37
AX625164/c
LOCUS       AX625164                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2205 from Patent WO02053774.
ACCESSION   AX625164
VERSION     AX625164.1  GI:28453105
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2205 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      2 c      4 g      4 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAA 16
              |||||||||
Db         11 CCAGGCCAA 3


RESULT 38
AX625382/c
LOCUS       AX625382                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2423 from Patent WO02053774.
ACCESSION   AX625382
VERSION     AX625382.1  GI:28453323
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2423 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||||||||
Db         11 GGCCAGGCC 3


RESULT 39
AX629145/c
LOCUS       AX629145                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6186 from Patent WO02053774.
ACCESSION   AX629145
VERSION     AX629145.1  GI:28457183
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6186 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      3 c      5 g      3 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAA 16
              |||||||||
Db         11 CCAGGCCAA 3


RESULT 40
AX629339/c
LOCUS       AX629339                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6380 from Patent WO02053774.
ACCESSION   AX629339
VERSION     AX629339.1  GI:28457377
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6380 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      2 c      5 g      4 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAA 16
              |||||||||
Db         10 CCAGGCCAA 2


RESULT 41
AX631056/c
LOCUS       AX631056                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8097 from Patent WO02053774.
ACCESSION   AX631056
VERSION     AX631056.1  GI:28459098
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8097 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      2 c      3 g      5 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAA 17
              |||||||||
Db         10 CAGGCCAAA 2


RESULT 42
AX632585/c
LOCUS       AX632585                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9627 from Patent WO02053774.
ACCESSION   AX632585
VERSION     AX632585.1  GI:28468200
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9627 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      2 c      4 g      4 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAA 16
              |||||||||
```

```
Db         11 CCAGGCCAA 3


RESULT 43
AR107817/c
LOCUS       AR107817                  10 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 63 from patent US 6110667.
ACCESSION   AR107817
VERSION     AR107817.1  GI:12823304
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
  TITLE     Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
  JOURNAL   Patent: US 6110667-A 63 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        0 a      4 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||||||
Db         10 CAGGCCAGGC 1


RESULT 44
AX152505/c
LOCUS       AX152505                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 420 from Patent WO0138577.
ACCESSION   AX152505
VERSION     AX152505.1  GI:14534156
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 420 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      5 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 45
AX152506/c
LOCUS       AX152506                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 421 from Patent WO0138577.
ACCESSION   AX152506
VERSION     AX152506.1  GI:14534157
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 421 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      5 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 46
AX152507
LOCUS       AX152507                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 422 from Patent WO0138577.
ACCESSION   AX152507
VERSION     AX152507.1  GI:14534158
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 422 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      4 g      0 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              |||||||| |
Db          1 GGCCAAAGGC 10


RESULT 47
AX152729
LOCUS       AX152729                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 644 from Patent WO0138577.
ACCESSION   AX152729
VERSION     AX152729.1  GI:14534380
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 644 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
```

```
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
BASE COUNT        5 a      2 c      2 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10


RESULT 48
AX153313/c
LOCUS       AX153313                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1228 from Patent WO0138577.
ACCESSION   AX153313
VERSION     AX153313.1  GI:14534964
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1228 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 49
AX153314/c
LOCUS       AX153314                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1229 from Patent WO0138577.
ACCESSION   AX153314
VERSION     AX153314.1  GI:14534965
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1229 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 50
AX153315/c
LOCUS       AX153315                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1230 from Patent WO0138577.
ACCESSION   AX153315
VERSION     AX153315.1  GI:14534966
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1230 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 51
AX153316/c
LOCUS       AX153316                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1231 from Patent WO0138577.
ACCESSION   AX153316
VERSION     AX153316.1  GI:14534967
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1231 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 52
AX153317/c
LOCUS       AX153317                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1232 from Patent WO0138577.
```

```
ACCESSION   AX153317
VERSION     AX153317.1  GI:14534968
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1232 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 53
AX153318/c
LOCUS       AX153318                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1233 from Patent WO0138577.
ACCESSION   AX153318
VERSION     AX153318.1  GI:14534969
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1233 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 54
AX153319/c
LOCUS       AX153319                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1234 from Patent WO0138577.
ACCESSION   AX153319
VERSION     AX153319.1  GI:14534970
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1234 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 55
AX224404/c
LOCUS       AX224404                 10 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 11 from Patent WO0160997.
ACCESSION   AX224404
VERSION     AX224404.1  GI:15554646
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
  TITLE     Male tissue-preferred regulatory region and method of using same
  JOURNAL   Patent: WO 0160997-A 11 23-AUG-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
BASE COUNT        0 a      5 c      5 g      0 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| |||
Db         10 CGGGCCCGGC 1


RESULT 56
AX224407
LOCUS       AX224407                 10 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 14 from Patent WO0160997.
ACCESSION   AX224407
VERSION     AX224407.1  GI:15554649
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
  TITLE     Male tissue-preferred regulatory region and method of using same
  JOURNAL   Patent: WO 0160997-A 14 23-AUG-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
```

```
                     /db_xref="taxon:4577"
BASE COUNT        0 a      5 c      5 g      0 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| ||| .
Db          1 CGGGCCCGGC 10


RESULT 57
AX224410/c
LOCUS       AX224410                  10 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 17 from Patent WO0160997.
ACCESSION   AX224410
VERSION     AX224410.1  GI:15554652
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
  TITLE     Male tissue-preferred regulatory region and method of using same
  JOURNAL   Patent: WO 0160997-A 17 23-AUG-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
BASE COUNT        0 a      5 c      5 g      0 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||||| ||||
Db         10 GGGCCCGGCC 1


RESULT 58
AX301480/c
LOCUS       AX301480                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 194 from Patent WO0185941.
ACCESSION   AX301480
VERSION     AX301480.1  GI:17382563
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 194 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      5 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 59
BD007979/c
LOCUS       BD007979                  10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007979
VERSION     BD007979.1  GI:18636352
KEYWORDS    JP 2001069993-A/255.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 255 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/255
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 60
BD065145/c
LOCUS       BD065145                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065145
VERSION     BD065145.1  GI:22610748
KEYWORDS    JP 2001509017-A/81.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 81 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/81
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
            C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
```

```
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Saccharomyces cerevisiae"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:4932"
BASE COUNT         0 a      5 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              ||||||| ||
Db         10 GGCCAGGGCA 1


RESULT 61
BD083124/c
LOCUS       BD083124                 10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human matured/activated dendritic cell expression genes.
ACCESSION   BD083124
VERSION     BD083124.1  GI:22628734
KEYWORDS    JP 2001327293-A/45.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
  TITLE     Human matured/activated dendritic cell expression genes
  JOURNAL   Patent: JP 2001327293-A 45 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001327293-A/45
            PD   27-NOV-2001
            PF   22-MAY-2000 JP 2000150562
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
              NAGAI
            PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT         1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 62
BD161262/c
LOCUS       BD161262                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161262
VERSION     BD161262.1  GI:27867020
KEYWORDS    JP 2002186482-A/84.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 84 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/84
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT         1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 63
BD166487
LOCUS       BD166487                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166487
VERSION     BD166487.1  GI:27872299
KEYWORDS    JP 2002209591-A/32.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 32 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/32
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
BASE COUNT         5 a      2 c      2 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10
```

```
RESULT 64
BD166906/c
LOCUS       BD166906                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166906
VERSION     BD166906.1  GI:27872718
KEYWORDS    JP 2002209591-A/451.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 451 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/451
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      2 c      3 g      4 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              |||||||| |
Db         10 AGGCCAAACT 1


RESULT 65
BD167212/c
LOCUS       BD167212                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167212
VERSION     BD167212.1  GI:27873024
KEYWORDS    JP 2002209591-A/757.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 757 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/757
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 66
E39489/c
LOCUS       E39489                   10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genes with human dendritic cell expression.
ACCESSION   E39489
VERSION     E39489.1  GI:18621580
KEYWORDS    JP 2000279181-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
  TITLE     Genes with human dendritic cell expression
  JOURNAL   Patent: JP 2000279181-A 22 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000279181-A/22
            PD   10-OCT-2000
            PF   01-APR-1999 JP 1999095481
            PR
            PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 67
E39743/c
LOCUS       E39743                   10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genes with human dendritic cell expression.
ACCESSION   E39743
VERSION     E39743.1  GI:18621834
KEYWORDS    JP 2000279181-A/276.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
  TITLE     Genes with human dendritic cell expression
  JOURNAL   Patent: JP 2000279181-A 276 10-OCT-2000;
```

```
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000279181-A/276
            PD   10-OCT-2000
            PF   01-APR-1999 JP 1999095481
            PR
            PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 68
E54829/c
LOCUS       E54829                    10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human normal liver cell expression genes.
ACCESSION   E54829
VERSION     E54829.1  GI:22556312
KEYWORDS    JP 2001211883-A/181.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human normal liver cell expression genes
  JOURNAL   Patent: JP 2001211883-A 181 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001211883-A/181
            PD   07-AUG-2001
            PF   31-JAN-2000 JP 2000023170
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K16/18,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 69
AX623125
LOCUS       AX623125                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 166 from Patent WO02053774.
ACCESSION   AX623125
VERSION     AX623125.1  GI:28451066
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 166 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      5 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || |||||||
Db          2 CCTGGCCAGG 11


RESULT 70
AX630546
LOCUS       AX630546                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7587 from Patent WO02053774.
ACCESSION   AX630546
VERSION     AX630546.1  GI:28458584
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7587 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      5 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || |||||||
Db          2 CCTGGCCAGG 11


RESULT 71
AX393189
LOCUS       AX393189                  11 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 119 from Patent WO0210217.
ACCESSION   AX393189
VERSION     AX393189.1  GI:19701239
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   St Croix,B., Kinzler,K.W. and Vogelstein,B.
```

```
  TITLE     Endothelial cell expression patterns
  JOURNAL   Patent: WO 0210217-A 119 07-FEB-2002;
            The Johns Hopkins University (US).
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      3 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGCCCAAAGT 10


RESULT 72
AX470637
LOCUS       AX470637                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 214 from Patent WO02053773.
ACCESSION   AX470637
VERSION     AX470637.1  GI:22205762
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 214 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              ||||| ||||
Db          2 AGGCCCAAGT 11


RESULT 73
AX470751/c
LOCUS       AX470751                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 328 from Patent WO02053773.
ACCESSION   AX470751
VERSION     AX470751.1  GI:22205876
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 328 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      4 c      5 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||||| |
Db         11 GCCAGGCCCA 2


RESULT 74
AX471339
LOCUS       AX471339                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 916 from Patent WO02053773.
ACCESSION   AX471339
VERSION     AX471339.1  GI:22206464
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 916 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      2 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              || |||||||
Db          1 CCTGGCCAAA 10


RESULT 75
AX471385
LOCUS       AX471385                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 962 from Patent WO02053773.
ACCESSION   AX471385
VERSION     AX471385.1  GI:22206510
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 962 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      2 c      3 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10
```

```
RESULT 76
AX482027
LOCUS       AX482027                  11 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 4 from Patent EP1225233.
ACCESSION   AX482027
VERSION     AX482027.1  GI:22316749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1225233-A 4 24-JUL-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TAG sequence Hs78436"
BASE COUNT        3 a      4 c      4 g      0 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              |||||||| |
Db          1 GGCCAAAGGC 10


RESULT 77
AX511266
LOCUS       AX511266                  11 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 4 from Patent WO02059558.
ACCESSION   AX511266
VERSION     AX511266.1  GI:23392143
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: WO 02059558-A 4 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TAG sequence Hs78436"
BASE COUNT        3 a      4 c      4 g      0 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              |||||||| |
Db          1 GGCCAAAGGC 10


RESULT 78
AX623296/c
LOCUS       AX623296                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 337 from Patent WO02053774.
ACCESSION   AX623296
VERSION     AX623296.1  GI:28451237
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 337 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      2 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 79
AX623449
LOCUS       AX623449                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 490 from Patent WO02053774.
ACCESSION   AX623449
VERSION     AX623449.1  GI:28451390
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 490 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              || |||||||
Db          1 GGCCCAGGCC 10


RESULT 80
AX623782
LOCUS       AX623782                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 823 from Patent WO02053774.
ACCESSION   AX623782
VERSION     AX623782.1  GI:28451723
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 823 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
```

```
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      2 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              || |||||||
Db          1 CCTGGCCAAA 10


RESULT 81
AX625842
LOCUS       AX625842                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2883 from Patent WO02053774.
ACCESSION   AX625842
VERSION     AX625842.1  GI:28453878
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2883 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||||||
Db          1 CTGGCCAGGC 10


RESULT 82
AX625891
LOCUS       AX625891                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2932 from Patent WO02053774.
ACCESSION   AX625891
VERSION     AX625891.1  GI:28453929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2932 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      5 g      0 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db          2 GAGCCAGGCC 11


RESULT 83
AX626383/c
LOCUS       AX626383                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3424 from Patent WO02053774.
ACCESSION   AX626383
VERSION     AX626383.1  GI:28454421
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3424 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      3 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              ||||||| ||
Db         10 GGCCAAACTC 1


RESULT 84
AX626723
LOCUS       AX626723                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3764 from Patent WO02053774.
ACCESSION   AX626723
VERSION     AX626723.1  GI:28454761
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3764 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      2 c      3 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10


RESULT 85
AX626887/c
LOCUS       AX626887                  11 bp    DNA     linear   PAT 21-FEB-2003
```

```
DEFINITION  Sequence 3928 from Patent WO02053774.
ACCESSION   AX626887
VERSION     AX626887.1  GI:28454925
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3928 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              ||||| ||||
Db         10 GGCCAGAGTC 1


RESULT 86
AX627709/c
LOCUS       AX627709                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4750 from Patent WO02053774.
ACCESSION   AX627709
VERSION     AX627709.1  GI:28455747
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4750 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      3 c      5 g      3 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCCGGCCAA 1


RESULT 87
AX628172/c
LOCUS       AX628172                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5213 from Patent WO02053774.
ACCESSION   AX628172
VERSION     AX628172.1  GI:28456210
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5213 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      5 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              || |||||||
Db         11 GGCCCAGGCC 2


RESULT 88
AX628292
LOCUS       AX628292                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5333 from Patent WO02053774.
ACCESSION   AX628292
VERSION     AX628292.1  GI:28456330
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5333 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              ||||| ||||
Db          2 AGGCCCAAGT 11


RESULT 89
AX629263/c
LOCUS       AX629263                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6304 from Patent WO02053774.
ACCESSION   AX629263
VERSION     AX629263.1  GI:28457301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6304 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
```

```
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              || |||||||
Db         10 TCGGGGCCAG 1


RESULT 90
AX629507/c
LOCUS       AX629507                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6548 from Patent WO02053774.
ACCESSION   AX629507
VERSION     AX629507.1  GI:28457545
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6548 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      3 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 91
AX629798
LOCUS       AX629798                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6839 from Patent WO02053774.
ACCESSION   AX629798
VERSION     AX629798.1  GI:28457836
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6839 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      4 c      4 g      0 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              |||||||| |
Db          1 GGCCAAAGGC 10


RESULT 92
AX629883/c
LOCUS       AX629883                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6924 from Patent WO02053774.
ACCESSION   AX629883
VERSION     AX629883.1  GI:28457921
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6924 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      4 c      5 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||||| |
Db         11 GCCAGGCCCA 2


RESULT 93
AX630156/c
LOCUS       AX630156                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7197 from Patent WO02053774.
ACCESSION   AX630156
VERSION     AX630156.1  GI:28458194
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7197 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      3 c      5 g      3 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||||| |
Db         10 GCCAGGCCCA 1


RESULT 94
AX630273/c
LOCUS       AX630273                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7314 from Patent WO02053774.
ACCESSION   AX630273
VERSION     AX630273.1  GI:28458311
KEYWORDS    .
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7314 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      4 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||||||| ||
Db         10 GGGCCAGTCC 1


RESULT 95
AX630717/c
LOCUS       AX630717                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7758 from Patent WO02053774.
ACCESSION   AX630717
VERSION     AX630717.1  GI:28458755
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7758 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 96
AX630870
LOCUS       AX630870                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7911 from Patent WO02053774.
ACCESSION   AX630870
VERSION     AX630870.1  GI:28458910
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7911 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              || |||||||
Db          1 GGCCCAGGCC 10


RESULT 97
AX631203
LOCUS       AX631203                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8245 from Patent WO02053774.
ACCESSION   AX631203
VERSION     AX631203.1  GI:28459249
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8245 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      2 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              || |||||||
Db          1 CCTGGCCAAA 10


RESULT 98
BD135851/c
LOCUS       BD135851                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Selective regulation of adenovirus production.
ACCESSION   BD135851
VERSION     BD135851.1  GI:23230796
KEYWORDS    JP 2002506355-A/22.
SOURCE      unidentified adenovirus
  ORGANISM  unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Hearing,P., Schmid,S.I., Ostapchuk,P.H. and Erturk,E.
  TITLE     Selective regulation of adenovirus production
  JOURNAL   Patent: JP 2002506355-A 22 26-FEB-2002;
            THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
COMMENT     OS   Adenovirus
            PN   JP 2002506355-A/22
            PD   26-FEB-2002
            PF   15-APR-1999 JP 1999552110
            PR   15-APR-1998 US    60/081867,05-JUN-1998 US    60/088321 PI
            PATRICK HEARING,SUSANNE I SCHMID,PHILONIENA H OSTAPCHUK,ECE  PI
            ERTURK
            PC   C12N15/86
            CC   COUP-TF SITE
            FH   Key             Location/Qualifiers
```

```
           FT   source          1. .11
           FT                   /organism='Adenovirus'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified adenovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10535"
BASE COUNT        2 a      3 c      3 g      3 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              || |||||||
Db         11 GGTCAAAGTC 2


RESULT 99
A94680/c
LOCUS       A94680                    9 bp    DNA     linear   PAT 26-JAN-2000
DEFINITION  Sequence 2 from Patent EP0939122.
ACCESSION   A94680
VERSION     A94680.1  GI:6778951
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   .
  TITLE     Mouse TCF-3 and TCF-4 and tumorigenesis related to WNT/Wingless
            signalling
  JOURNAL   Patent: EP 0939122-A 2 01-SEP-1999;
            UNIV UTRECHT (NL)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        0 a      4 c      2 g      3 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAG 18
              ||||||||
Db          9 GGCCAAAG 2


RESULT 100
AX023498/c
LOCUS       AX023498                  9 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 2 from Patent WO0018913.
ACCESSION   AX023498
VERSION     AX023498.1  GI:10183893
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   van Es,J.H., Clevers,J.C. and Pelfer,M.A.
  TITLE     Apc-2
  JOURNAL   Patent: WO 0018913-A 2 06-APR-2000;
            ES JOHANNES HENDRIKUS VAN (NL) ; UNIV UTRECHT (NL) ; CLEVERS
            JOHANNES CAROLUS (NL) ; PELFER MARK ALAN (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="mutation Fcf-responsive element"
BASE COUNT        0 a      4 c      2 g      3 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAG 18
              ||||||||
Db          9 GGCCAAAG 2


RESULT 101
AX668925/c
LOCUS       AX668925                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2374 from Patent WO0242459.
ACCESSION   AX668925
VERSION     AX668925.1  GI:29291902
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2374 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        0 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 102
AX668927/c
LOCUS       AX668927                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2376 from Patent WO0242459.
ACCESSION   AX668927
VERSION     AX668927.1  GI:29291904
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2376 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        0 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
```

```
Db          9 CCAGGCCA 2


RESULT 103
AX668975/c
LOCUS       AX668975                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2424 from Patent WO0242459.
ACCESSION   AX668975
VERSION     AX668975.1  GI:29291952
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2424 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        0 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 104
AX153313
LOCUS       AX153313                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1228 from Patent WO0138577.
ACCESSION   AX153313
VERSION     AX153313.1  GI:14534964
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1228 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 105
AX153314
LOCUS       AX153314                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1229 from Patent WO0138577.
ACCESSION   AX153314
VERSION     AX153314.1  GI:14534965
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1229 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 106
AX153315
LOCUS       AX153315                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1230 from Patent WO0138577.
ACCESSION   AX153315
VERSION     AX153315.1  GI:14534966
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1230 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 107
AX153316
LOCUS       AX153316                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1231 from Patent WO0138577.
ACCESSION   AX153316
VERSION     AX153316.1  GI:14534967
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
```

```
  JOURNAL   Patent: WO 0138577-A 1231 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match           40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 108
AX153317
LOCUS       AX153317                10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1232 from Patent WO0138577.
ACCESSION   AX153317
VERSION     AX153317.1  GI:14534968
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1232 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match           40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 109
AX153318
LOCUS       AX153318                10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1233 from Patent WO0138577.
ACCESSION   AX153318
VERSION     AX153318.1  GI:14534969
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1233 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match           40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 110
AX153319
LOCUS       AX153319                10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1234 from Patent WO0138577.
ACCESSION   AX153319
VERSION     AX153319.1  GI:14534970
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1234 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match           40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 111
BD083124
LOCUS       BD083124                10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human matured/activated dendritic cell expression genes.
ACCESSION   BD083124
VERSION     BD083124.1  GI:22628734
KEYWORDS    JP 2001327293-A/45.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
  TITLE     Human matured/activated dendritic cell expression genes
  JOURNAL   Patent: JP 2001327293-A 45 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001327293-A/45
            PD   27-NOV-2001
            PF   22-MAY-2000 JP 2000150562
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
              NAGAI
            PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t
```

```
  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 112
BD161262
LOCUS       BD161262                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161262
VERSION     BD161262.1  GI:27867020
KEYWORDS    JP 2002186482-A/84.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 84 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/84
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 113
BD167212
LOCUS       BD167212                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167212
VERSION     BD167212.1  GI:27873024
KEYWORDS    JP 2002209591-A/757.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 757 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/757
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 114
E39489
LOCUS       E39489                    10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genes with human dendritic cell expression.
ACCESSION   E39489
VERSION     E39489.1  GI:18621580
KEYWORDS    JP 2000279181-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
  TITLE     Genes with human dendritic cell expression
  JOURNAL   Patent: JP 2000279181-A 22 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000279181-A/22
            PD   10-OCT-2000
            PF   01-APR-1999 JP 1999095481
            PR
            PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 115
E54829
LOCUS       E54829                    10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human normal liver cell expression genes.
ACCESSION   E54829
VERSION     E54829.1  GI:22556312
KEYWORDS    JP 2001211883-A/181.
SOURCE      Homo sapiens (human)
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human normal liver cell expression genes
  JOURNAL   Patent: JP 2001211883-A 181 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001211883-A/181
            PD   07-AUG-2001
            PF   31-JAN-2000 JP 2000023170
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K16/18,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      2 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 116
AR058606/c
LOCUS       AR058606                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 183 from patent US 5837832.
ACCESSION   AR058606
VERSION     AR058606.1  GI:5984183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
            Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
  TITLE     Arrays of nucleic acid probes on biological chips
  JOURNAL   Patent: US 5837832-A 183 17-NOV-1998;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
BASE COUNT        1 a      4 c      5 g      0 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCC 9
              ||||||||
Db          8 TCCGGGCC 1


RESULT 117
AR088590/c
LOCUS       AR088590                  10 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from patent US 5989906.
ACCESSION   AR088590
VERSION     AR088590.1  GI:10015354
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Thompson,J.D.
  TITLE     Method and reagent for inhibiting P-glycoprotein (mdr-1-gene)
  JOURNAL   Patent: US 5989906-A 6 23-NOV-1999;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
BASE COUNT        2 a      2 c      3 g      3 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAGT 19
              ||||||||
Db         10 GCCAAAGT 3


RESULT 118
AX152706
LOCUS       AX152706                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 621 from Patent WO0138577.
ACCESSION   AX152706
VERSION     AX152706.1  GI:14534357
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 621 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      2 c      7 g      0 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          1 GGGCCAGG 8


RESULT 119
AX152961/c
LOCUS       AX152961                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 876 from Patent WO0138577.
ACCESSION   AX152961
VERSION     AX152961.1  GI:14534612
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 876 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
```

```
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 120
AX152962/c
LOCUS       AX152962                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 877 from Patent WO0138577.
ACCESSION   AX152962
VERSION     AX152962.1  GI:14534613
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 877 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 121
AX153299/c
LOCUS       AX153299                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1214 from Patent WO0138577.
ACCESSION   AX153299
VERSION     AX153299.1  GI:14534950
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1214 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      3 g      2 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 122
AX153300/c
LOCUS       AX153300                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1215 from Patent WO0138577.
ACCESSION   AX153300
VERSION     AX153300.1  GI:14534951
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1215 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      3 g      2 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 123
BD007922
LOCUS       BD007922                  10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007922
VERSION     BD007922.1  GI:18636295
KEYWORDS    JP 2001069993-A/198.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 198 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/198
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      2 c      7 g      0 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
```

```
Db          1 GGGCCAGG 8


RESULT 124
BD007953/c
LOCUS       BD007953                  10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007953
VERSION     BD007953.1  GI:18636326
KEYWORDS    JP 2001069993-A/229.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 229 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/229
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT         1 a      4 c      3 g      2 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 125
BD083213
LOCUS       BD083213                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human matured/activated dendritic cell expression genes.
ACCESSION   BD083213
VERSION     BD083213.1  GI:22628823
KEYWORDS    JP 2001327293-A/134.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
  TITLE     Human matured/activated dendritic cell expression genes
  JOURNAL   Patent: JP 2001327293-A 134 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001327293-A/134
            PD   27-NOV-2001
            PF   22-MAY-2000 JP 2000150562
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
              NAGAI
            PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT         3 a      3 c      4 g      0 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAA 16
              ||||||||
Db          2 CAGGCCAA 9


RESULT 126
BD083308/c
LOCUS       BD083308                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human matured/activated dendritic cell expression genes.
ACCESSION   BD083308
VERSION     BD083308.1  GI:22628918
KEYWORDS    JP 2001327293-A/229.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
  TITLE     Human matured/activated dendritic cell expression genes
  JOURNAL   Patent: JP 2001327293-A 229 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001327293-A/229
            PD   27-NOV-2001
            PF   22-MAY-2000 JP 2000150562
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
              NAGAI
            PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT         1 a      4 c      4 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAG 11
              ||||||||
Db          8 CGGGCCAG 1


RESULT 127
BD161348
LOCUS       BD161348                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161348
VERSION     BD161348.1  GI:27867106
KEYWORDS    JP 2002186482-A/170.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 170 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
```

```
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/170
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      2 c      4 g      0 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAG 18
               ||||||||
Db          1 GGCCAAAG 8


RESULT 128
BD166572
LOCUS       BD166572                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166572
VERSION     BD166572.1  GI:27872384
KEYWORDS    JP 2002209591-A/117.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 117 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/117
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      2 c      3 g      0 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAA 17
               ||||||||
Db          2 AGGCCAAA 9


RESULT 129
BD167054
LOCUS       BD167054                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167054
VERSION     BD167054.1  GI:27872866
KEYWORDS    JP 2002209591-A/599.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 599 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/599
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      2 c      6 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
               ||||||||
Db          3 GGGCCAGG 10


RESULT 130
E54715
LOCUS       E54715                   10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human normal liver cell expression genes.
ACCESSION   E54715
VERSION     E54715.1  GI:22556198
KEYWORDS    JP 2001211883-A/67.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human normal liver cell expression genes
  JOURNAL   Patent: JP 2001211883-A 67 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001211883-A/67
            PD   07-AUG-2001
            PF   31-JAN-2000 JP 2000023170
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K16/18,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      4 g      0 t
```

```
  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAA 16
              ||||||||
Db          2 CAGGCCAA 9


RESULT 131
AX482038
LOCUS       AX482038                  11 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 15 from Patent EP1225233.
ACCESSION   AX482038
VERSION     AX482038.1  GI:22316760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1225233-A 15 24-JUL-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TAG sequence Hs74649 and Hs288761"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCC 14
              | |||| ||||
Db          1 CAGGCCTGGCC 11


RESULT 132
AX511277
LOCUS       AX511277                  11 bp    DNA     linear   PAT 28-SEP-2002
DEFINITION  Sequence 15 from Patent WO02059558.
ACCESSION   AX511277
VERSION     AX511277.1  GI:23392154
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: WO 02059558-A 15 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TAG sequence Hs74649 and Hs288761"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCC 14
              | |||| ||||
Db          1 CAGGCCTGGCC 11


RESULT 133
AX625382
LOCUS       AX625382                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2423 from Patent WO02053774.
ACCESSION   AX625382
VERSION     AX625382.1  GI:28453323
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2423 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      4 g      1 t

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCC 14
              | |||| ||||
Db          1 CAGGCCTGGCC 11


RESULT 134
AX470751
LOCUS       AX470751                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 328 from Patent WO02053773.
ACCESSION   AX470751
VERSION     AX470751.1  GI:22205876
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 328 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      4 c      5 g      2 t

  Query Match            39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              | ||||| |||
Db          1 CTGGGCCTGGC 11


RESULT 135
AX629883
LOCUS       AX629883                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6924 from Patent WO02053774.
ACCESSION   AX629883
VERSION     AX629883.1  GI:28457921
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6924 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      4 c      5 g      2 t

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              | ||||| |||
Db          1 CTGGGCCTGGC 11


RESULT 136
AR145684/c
LOCUS       AR145684                  17 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6218109.
ACCESSION   AR145684
VERSION     AR145684.1  GI:15108873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Elledge,S.J. and Sanchez,Y.
  TITLE     Mammalian checkpoint genes and proteins
  JOURNAL   Patent: US 6218109-A 6 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      4 c      5 g      3 t

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 137
AR174508/c
LOCUS       AR174508                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 6 from patent US 6307015.
ACCESSION   AR174508
VERSION     AR174508.1  GI:17914828
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Elledge,S.J. and Sanchez,Y.
  TITLE     Mammalian checkpoint genes and proteins
  JOURNAL   Patent: US 6307015-A 6 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      4 c      5 g      3 t

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 138
AR110470/c
LOCUS       AR110470                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 7 from patent US 6114517.
ACCESSION   AR110470
VERSION     AR110470.1  GI:12826746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Xu,X.S.
  TITLE     Methods of modulating tumor necrosis factor .alpha.-induced
            expression of cell adhesion molecules
  JOURNAL   Patent: US 6114517-A 7 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 139
AR116450/c
LOCUS       AR116450                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6133246.
ACCESSION   AR116450
VERSION     AR116450.1  GI:14096772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 31 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 140
AR116461
LOCUS       AR116461                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 42 from patent US 6133246.
ACCESSION   AR116461
VERSION     AR116461.1  GI:14096783
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

```
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 42 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        2 a      7 c      7 g      4 t

  Query Match            38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db          7 GGCCTGGCCCGGAC 20


RESULT 141
AX104119/c
LOCUS       AX104119                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 311 from Patent WO0122972.
ACCESSION   AX104119
VERSION     AX104119.1  GI:13920316
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 311 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match            38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 142
AX164692/c
LOCUS       AX164692                  20 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0134792.
ACCESSION   AX164692
VERSION     AX164692.1  GI:14545586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Potapova,O., Gorospe,M. and Holbrook,N.J.
  TITLE     Compositions and methods for the diminution or elimination of
            various cancers
  JOURNAL   Patent: WO 0134792-A 2 17-MAY-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match            38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 143
AX355435/c
LOCUS       AX355435                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 463 from Patent WO0197843.
ACCESSION   AX355435
VERSION     AX355435.1  GI:18620103
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 463 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match            38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 144
AX547172/c
LOCUS       AX547172                  20 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 311 from Patent WO02053141.
ACCESSION   AX547172
VERSION     AX547172.1  GI:25812316
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 311 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match            38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 145
BD074607/c
LOCUS       BD074607                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisence oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION   BD074607
VERSION     BD074607.1  GI:22620210
KEYWORDS    JP 2001514905-A/31.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mckay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
  TITLE     Antisence oligonucleotide composition and modulation method of JNK
            protein
  JOURNAL   Patent: JP 2001514905-A 31 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514905-A/31
            PD   18-SEP-2001
            PF   07-AUG-1998 JP 2000509875
            PR   13-AUG-1997 US    08/910629
            PI   ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO,WILLIAM A GAARDE
            PC   C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC   C12N15/00
            CC   antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match            38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 146
BD074618
LOCUS       BD074618                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisence oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION   BD074618
VERSION     BD074618.1  GI:22620221
KEYWORDS    JP 2001514905-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mckay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
  TITLE     Antisence oligonucleotide composition and modulation method of JNK
            protein
  JOURNAL   Patent: JP 2001514905-A 42 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514905-A/42
            PD   18-SEP-2001
            PF   07-AUG-1998 JP 2000509875
            PR   13-AUG-1997 US    08/910629
            PI   ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO,WILLIAM A GAARDE
            PC   C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC   C12N15/00
            CC   control sequence (sense)
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        2 a      7 c      7 g      4 t

  Query Match            38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db          7 GGCCTGGCCCGGAC 20


RESULT 147
AX205250
LOCUS       AX205250                  9 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 142 from Patent WO0155369.
ACCESSION   AX205250
VERSION     AX205250.1  GI:15394509
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Mauro,V.P., Edelman,G.M., Chappell,G.M., Owens,G., Pinkstaff,J.K.,
            Krushel,L. and Zhou,W.
  TITLE     Synthetic internal ribosome entry sites and methods of identifying
            same
  JOURNAL   Patent: WO 0155369-A 142 02-AUG-2001;
            The Scripps Research Institute (US) ; The Neurosciences Institute
            (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="random 9 nt sequence"
BASE COUNT        1 a      3 c      4 g      1 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity  88.9%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCC 9
              |||||||||
Db          1 GTCCGGGAC 9


RESULT 148
AX668699
LOCUS       AX668699                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2148 from Patent WO0242459.
ACCESSION   AX668699
VERSION     AX668699.1  GI:29291674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
```

```
  JOURNAL   Patent: WO 0242459-A 2148 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      6 g      0 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 149
AX668700
LOCUS       AX668700                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2149 from Patent WO0242459.
ACCESSION   AX668700
VERSION     AX668700.1  GI:29291675
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2149 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      6 g      0 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 150
AX224404
LOCUS       AX224404                 10 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 11 from Patent WO0160997.
ACCESSION   AX224404
VERSION     AX224404.1  GI:15554646
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
  TITLE     Male tissue-preferred regulatory region and method of using same
  JOURNAL   Patent: WO 0160997-A 11 23-AUG-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
BASE COUNT        0 a      5 c      5 g      0 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAG 11
              ||||||| |
Db          2 CCGGGCCCG 10


RESULT 151
AX224407/c
LOCUS       AX224407                 10 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 14 from Patent WO0160997.
ACCESSION   AX224407
VERSION     AX224407.1  GI:15554649
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
  TITLE     Male tissue-preferred regulatory region and method of using same
  JOURNAL   Patent: WO 0160997-A 14 23-AUG-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
BASE COUNT        0 a      5 c      5 g      0 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAG 11
              ||||||| |
Db          9 CCGGGCCCG 1


RESULT 152
AX224410
LOCUS       AX224410                 10 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 17 from Patent WO0160997.
ACCESSION   AX224410
VERSION     AX224410.1  GI:15554652
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
  TITLE     Male tissue-preferred regulatory region and method of using same
  JOURNAL   Patent: WO 0160997-A 17 23-AUG-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
BASE COUNT        0 a      5 c      5 g      0 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          1 GTCCGGGCC 9
              | |||||||
Db          1 GGCCGGGCC 9


RESULT 153
AX153299
LOCUS       AX153299                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1214 from Patent WO0138577.
ACCESSION   AX153299
VERSION     AX153299.1  GI:14534950
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1214 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      3 g      2 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db          1 GCCTGGCCA 9


RESULT 154
AX153300
LOCUS       AX153300                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1215 from Patent WO0138577.
ACCESSION   AX153300
VERSION     AX153300.1  GI:14534951
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1215 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      3 g      2 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db          1 GCCTGGCCA 9


RESULT 155
BD007953
LOCUS       BD007953                 10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007953
VERSION     BD007953.1  GI:18636326
KEYWORDS    JP 2001069993-A/229.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 229 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/229
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      3 g      2 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 86;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db          1 GCCTGGCCA 9


RESULT 156
AX625842/c
LOCUS       AX625842                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2883 from Patent WO02053774.
ACCESSION   AX625842
VERSION     AX625842.1  GI:28453878
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2883 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      2 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 11;
  Best Local Similarity  88.9%;  Pred. No. 96;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db         10 GCCTGGCCA 2
```

```
RESULT 157
AX630156
LOCUS       AX630156                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7197 from Patent WO02053774.
ACCESSION   AX630156
VERSION     AX630156.1  GI:28458194
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7197 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      3 c      5 g      3 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 11;
  Best Local Similarity  88.9%;  Pred. No. 96;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||||| |||
Db          2 GGGCCTGGC 10


RESULT 158
AX129247
LOCUS       AX129247                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 465 from Patent WO0130362.
ACCESSION   AX129247
VERSION     AX129247.1  GI:14135552
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 465 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk4 ribozyme binding site"
BASE COUNT        1 a      6 c      7 g      5 t

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 19;
  Best Local Similarity  88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||| ||||
Db         11 GGCCTGGCC 19


RESULT 159
AX017438/c
LOCUS       AX017438                   9 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 13 from Patent WO9947656.
ACCESSION   AX017438
VERSION     AX017438.1  GI:10042250
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Isalan,M. and Choo,Y.
  TITLE     Nucleic acid binding proteins
  JOURNAL   Patent: WO 9947656-A 13 23-SEP-1999;
            MEDICAL RES COUNCIL (GB); ISALAN MARK (GB); CHOO YEN (GB)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      4 c      5 g      0 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CCGGGCC 9
              |||||||
Db          7 CCGGGCC 1


RESULT 160
AX538878/c
LOCUS       AX538878                   9 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 12 from Patent WO0208436.
ACCESSION   AX538878
VERSION     AX538878.1  GI:25271599
KEYWORDS    .
SOURCE      unidentified adenovirus
  ORGANISM  unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1
  AUTHORS   Zhang,W.W., Alemany,R., Dai,Y., Josephs,S., Balague,C., Ayares,D.
            and Schneiderman,R.
  TITLE     Mini-adenoviral vector system for vaccination
  JOURNAL   Patent: WO 0208436-A 12 31-JAN-2002;
            Genstar Therapeutics Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="unidentified adenovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10535"
     misc_feature    1. .9
                     /note="A repeat VI"
BASE COUNT        1 a      1 c      4 g      3 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 CAAAGTC 20
              |||||||
Db          9 CAAAGTC 3


RESULT 161
AX668947/c
LOCUS       AX668947                   9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2396 from Patent WO0242459.
ACCESSION   AX668947
VERSION     AX668947.1  GI:29291924
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2396 30-MAY-2002;
```

```
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      3 g      3 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          8 GCCAAAG 2


RESULT 162
AX668948/c
LOCUS       AX668948                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2397 from Patent WO0242459.
ACCESSION   AX668948
VERSION     AX668948.1  GI:29291925
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2397 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      3 g      3 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          8 GCCAAAG 2


RESULT 163
BD138429/c
LOCUS       BD138429                  9 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Nucleic acid binding proteins.
ACCESSION   BD138429
VERSION     BD138429.1  GI:23233374
KEYWORDS    JP 2002506640-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Choo,Y. and Isalan,M.
  TITLE     Nucleic acid binding proteins
  JOURNAL   Patent: JP 2002506640-A 4 05-MAR-2002;
            GENDAQ LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002506640-A/4
            PD   05-MAR-2002
            PF   17-MAR-1999 JP 2000536839
            PR   17-MAR-1998 GB    9805576.7,31-MAR-1998 GB    9806895.0 PR
            03-APR-1998 GB    9807246.5
            PI   YEN CHOO,MARK ISALAN
            PC   C12N15/09,C07K14/00,C12P21/02,C12N15/00
            CC   description of artificial sequence: Synthetic sequence FH
            Key             Location/Qualifiers
            FT   source          1. .9
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      4 c      5 g      0 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CCGGGCC 9
              |||||||
Db          7 CCGGGCC 1


RESULT 164
AX471339/c
LOCUS       AX471339                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 916 from Patent WO02053773.
ACCESSION   AX471339
VERSION     AX471339.1  GI:22206464
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 916 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      2 g      1 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGG 12
              |||||||
Db          7 GGCCAGG 1


RESULT 165
AX623782/c
LOCUS       AX623782                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 823 from Patent WO02053774.
ACCESSION   AX623782
VERSION     AX623782.1  GI:28451723
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 823 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
```

```
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      2 g      1 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGG 12
              |||||||
Db          7 GGCCAGG 1


RESULT 166
AX631203/c
LOCUS       AX631203                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8245 from Patent WO02053774.
ACCESSION   AX631203
VERSION     AX631203.1  GI:28459249
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8245 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      2 g      1 t

  Query Match            35.0%;  Score 7;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGG 12
              |||||||
Db          7 GGCCAGG 1


RESULT 167
AX152961
LOCUS       AX152961                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 876 from Patent WO0138577.
ACCESSION   AX152961
VERSION     AX152961.1  GI:14534612
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 876 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match            34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||  |||
Db          1 CAGGCCTGGC 10


RESULT 168
AX152962
LOCUS       AX152962                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 877 from Patent WO0138577.
ACCESSION   AX152962
VERSION     AX152962.1  GI:14534613
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 877 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match            34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||  |||
Db          1 CAGGCCTGGC 10


RESULT 169
AX629507
LOCUS       AX629507                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6548 from Patent WO02053774.
ACCESSION   AX629507
VERSION     AX629507.1  GI:28457545
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6548 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      3 g      2 t

  Query Match            34.0%;  Score 6.8;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              |||| | |||
Db          2 GGCCTGCCCA 11


RESULT 170
E63474
LOCUS       E63474                     8 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Non-human animal having modified foreign chromosomal or slice
            thereof.
ACCESSION   E63474
```

```
VERSION     E63474.1  GI:22557583
KEYWORDS    JP 2001231403-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Tomizuka,K., Yoshida,H., Ishida,I. and Kuroiwa,Y.
  TITLE     Non-human animal having modified foreign chromosomal or slice
  JOURNAL   Patent: JP 2001231403-A 6 28-AUG-2001;
            KIRIN BEER KK
COMMENT     OS   Artificial Sequence
            PN   JP 2001231403-A/6
            PD   28-AUG-2001
            PF   18-FEB-2000 JP 2000042074
            PI   KAZUMA TOMIZUKA,HITOSHI YOSHIDA,ISAO ISHIDA,YOSHIMI KUROIWA PC
              A01K67/027,C12N5/10,C12N15/09//(C12N5/10,C12R1:91),(C12N15/09, PC
              C12R1:91),
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91),(C12N15/00,C12R1:91) CC
              Description of Artificial Sequence: SrfI linker FH   Key
               Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      4 c      4 g      0 t

  Query Match            32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity  87.5%;  Pred. No. 3.3e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGC 8
              | ||||||
Db          1 GCCCGGGC 8


RESULT 171
E63474/c
LOCUS       E63474                    8 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Non-human animal having modified foreign chromosomal or slice
            thereof.
ACCESSION   E63474
VERSION     E63474.1  GI:22557583
KEYWORDS    JP 2001231403-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Tomizuka,K., Yoshida,H., Ishida,I. and Kuroiwa,Y.
  TITLE     Non-human animal having modified foreign chromosomal or slice
  JOURNAL   Patent: JP 2001231403-A 6 28-AUG-2001;
            KIRIN BEER KK
COMMENT     OS   Artificial Sequence
            PN   JP 2001231403-A/6
            PD   28-AUG-2001
            PF   18-FEB-2000 JP 2000042074
            PI   KAZUMA TOMIZUKA,HITOSHI YOSHIDA,ISAO ISHIDA,YOSHIMI KUROIWA PC
              A01K67/027,C12N5/10,C12N15/09//(C12N5/10,C12R1:91),(C12N15/09, PC
              C12R1:91),
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91),(C12N15/00,C12R1:91) CC
              Description of Artificial Sequence: SrfI linker FH   Key
               Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      4 c      4 g      0 t

  Query Match            32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity  87.5%;  Pred. No. 3.3e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGC 8
              | ||||||
Db          8 GCCCGGGC 1


Search completed: November 10, 2003, 07:57:04
Job time : 1 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 08:01:31 ; Search time 1 Seconds
(without alignments)
0.102 Million cell updates/sec

Title: us-09-774-809-31
Perfect score: 20
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 232 seqs, 2559 residues

Total number of hits satisfying chosen parameters: 464

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : rng.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	20	1	AAX29342	Chemically modifie
	2	20	100.0	20	1	AAX29331	JNK2-specific prob
	3	20	100.0	20	1	AAC62874	JNK antisense olig
c	4	20	100.0	20	1	AAC62885	JNK antisense olig
	5	20	100.0	20	1	AAA48651	Antisense oligonuc
	6	20	100.0	20	1	AAH23754	JNK1 antisense oli
	7	20	100.0	20	1	AAF99183	Immunostimulatory
	8	20	100.0	20	1	ABS77827	Angiogenesis inhib
	9	20	100.0	20	1	ABL39057	Immunostimulatory
	10	15.4	77.0	18	1	AAV60744	Primer #2 for huma
c	11	15	75.0	19	1	AAA82879	cdk4 ribozyme bind
c	12	15	75.0	19	1	AAH58041	Cell-cycle depende
c	13	14.8	74.0	18	1	AAX73494	Mouse flk-1 VEGF r
c	14	14.4	72.0	17	1	AAX71472	Human KDR VEGF rec
c	15	14	70.0	17	1	AAX74911	Mouse flt-1 VEGF r
c	16	13.4	67.0	17	1	AAX69246	Human flt1 VEGF re
	17	13.4	67.0	17	1	AAD03853	Human cell cycle c
	18	13.4	67.0	17	1	AAS18424	Degenerate PCR pri
	19	13.4	67.0	17	1	ABX16354	Human checkpoint g
c	20	13	65.0	17	1	AAX74910	Mouse flt-1 VEGF r
c	21	12.8	64.0	17	1	AAX73045	Mouse flk-1 VEGF r
	22	11.4	57.0	15	1	AAS19798	ASO primer #56 to
c	23	10.8	54.0	14	1	AAT76461	Chymase antisense
c	24	10.8	54.0	14	1	AAX54253	Chymase antisense
c	25	10.8	54.0	14	1	AAF19819	Human chymase poly
c	26	10.8	54.0	14	1	AAA33697	Low adenosine anti
	27	10.4	52.0	12	1	AAZ41523	Microbe detection
	28	10.4	52.0	12	1	AAZ41739	Organic material d
	29	10.4	52.0	12	1	AAC97874	Primer used to ill
c	30	10	50.0	10	1	AAZ81584	Metastatic breast
c	31	10	50.0	10	1	AAZ86676	Metastatic breast
c	32	10	50.0	10	1	AAH64570	Human ubiquitously
c	33	10	50.0	10	1	AAH64571	Human ubiquitously
	34	10	50.0	12	1	ABZ72939	Rod opsin hammerhe
c	35	9.8	49.0	13	1	AAV63772	Human JAGGED1 exon
c	36	9.8	49.0	13	1	AAA04950	Tenascin-C phospho
c	37	9.8	49.0	13	1	AAA05213	Tenascin-C phospho
c	38	9.8	49.0	13	1	ABC48592	Oligonucleotide SE
	39	9.8	49.0	13	1	ABC48593	Oligonucleotide SE
	40	9.4	47.0	11	1	AAZ19014	Murine MRL SAGE ta
c	41	9.4	47.0	11	1	AAX55034	C/EBP-beta antisen
c	42	9.4	47.0	11	1	AAF20603	Human C/EBP polynu
	43	9.4	47.0	11	1	AAC63229	Oligonucleotide #2
c	44	9.4	47.0	11	1	AAA34481	Human adenosine re
c	45	9.4	47.0	11	1	ABV62380	Human skin EST 166
c	46	9.4	47.0	11	1	ABV66640	Human skin EST 442
c	47	9.4	47.0	11	1	ABV69801	Human skin EST 758
c	48	9.4	47.0	12	1	AAX55033	C/EBP-beta antisen
c	49	9.4	47.0	12	1	AAF20602	Human C/EBP polynu
c	50	9.4	47.0	12	1	AAA34480	Human adenosine re
c	51	9	45.0	10	1	AAZ79191	Human dendritic ce
c	52	9	45.0	10	1	AAZ82328	Metastatic breast
	53	9	45.0	10	1	AAZ85483	Metastatic breast
c	54	9	45.0	10	1	AAZ86477	Metastatic breast
c	55	9	45.0	10	1	AAZ86559	Metastatic breast
c	56	9	45.0	10	1	ABL52193	Human PER1 preferr
c	57	9	45.0	10	1	AAS19877	Oligonucleotide #5
	58	9	45.0	10	1	AAD26166	Human endothelin 2
c	59	9	45.0	11	1	ABQ81865	Kaposi's Sarcoma S
c	60	9	45.0	11	1	ABV62890	Human skin EST 676
c	61	9	45.0	11	1	ABV64419	Human skin EST 220
c	62	9	45.0	11	1	ABV64637	Human skin EST 242
c	63	9	45.0	11	1	ABV68400	Human skin EST 618
c	64	9	45.0	11	1	ABV68594	Human skin EST 638
c	65	9	45.0	11	1	ABV70311	Human skin EST 809
c	66	9	45.0	11	1	ABV71840	Human skin EST 962
c	67	8.8	44.0	15	1	AAS19798	ASO primer #56 to
c	68	8.8	44.0	18	1	AAV60744	Primer #2 for huma
	69	8.4	42.0	10	1	AAQ96791	HIV-1 NL4-3 nef ge
c	70	8.4	42.0	10	1	AAT29327	5'-primer for mamm
c	71	8.4	42.0	10	1	AAV50125	Yeast tag for NORF
	72	8.4	42.0	10	1	AAX54917	C/EBP-beta antisen
	73	8.4	42.0	10	1	AAF20486	Human C/EBP polynu
c	74	8.4	42.0	10	1	AAC73935	Human dendritic ce
c	75	8.4	42.0	10	1	AAC74189	Human monocyte and
	76	8.4	42.0	10	1	AAA34364	Human adenosine re
c	77	8.4	42.0	10	1	AAZ77977	Human dendritic ce
	78	8.4	42.0	10	1	AAZ78898	Human dendritic ce
	79	8.4	42.0	10	1	AAZ81571	Metastatic breast
c	80	8.4	42.0	10	1	AAZ82444	Metastatic breast
c	81	8.4	42.0	10	1	AAZ82611	Metastatic breast
	82	8.4	42.0	10	1	AAZ82634	Metastatic breast
c	83	8.4	42.0	10	1	AAZ82905	Metastatic breast
c	84	8.4	42.0	10	1	AAZ83555	Metastatic breast
	85	8.4	42.0	10	1	AAZ84116	Metastatic breast
c	86	8.4	42.0	10	1	AAZ84369	Metastatic breast
	87	8.4	42.0	10	1	AAZ84683	Metastatic breast
c	88	8.4	42.0	10	1	AAZ84966	Metastatic breast
c	89	8.4	42.0	10	1	AAZ85815	Metastatic breast
	90	8.4	42.0	10	1	AAZ85951	Metastatic breast
c	91	8.4	42.0	10	1	AAZ86053	Metastatic breast
c	92	8.4	42.0	10	1	AAI67394	Human FKBP8 gene p
c	93	8.4	42.0	10	1	ABA06204	Human normal hepat
c	94	8.4	42.0	10	1	AAH76342	Z. mays Ms45 promo
	95	8.4	42.0	10	1	AAH76345	Z. mays Ms45 promo
c	96	8.4	42.0	10	1	AAH76348	Z. mays Ms45 promo
c	97	8.4	42.0	10	1	AAH63580	Human ubiquitously
c	98	8.4	42.0	10	1	AAH63581	Human ubiquitously
	99	8.4	42.0	10	1	AAH63582	Human ubiquitously
	100	8.4	42.0	10	1	AAH63804	Human ubiquitously
c	101	8.4	42.0	10	1	AAH64388	Human ubiquitously
c	102	8.4	42.0	10	1	AAH64389	Human ubiquitously
c	103	8.4	42.0	10	1	AAH64390	Human ubiquitously
c	104	8.4	42.0	10	1	AAH64391	Human ubiquitously
c	105	8.4	42.0	10	1	AAH64392	Human ubiquitously
c	106	8.4	42.0	10	1	AAH64393	Human ubiquitously

c 107	8.4	42.0	10	1	AAH64394	Human ubiquitously
c 108	8.4	42.0	10	1	AAH32882	LPS activated huma
c 109	8.4	42.0	10	1	AAF74058	Human SLC6A4 allel
c 110	8.4	42.0	10	1	AAF33342	Yeast NORF gene SA
c 111	8.4	42.0	10	1	AAF33708	Yeast NORF gene SA
c 112	8.4	42.0	10	1	AAF34406	Yeast NORF gene SA
c 113	8.4	42.0	10	1	AAF35939	Yeast NORF gene SA
c 114	8.4	42.0	10	1	AAF41896	Yeast NORF gene SA
115	8.4	42.0	10	1	AAF42385	Yeast NORF gene SA
c 116	8.4	42.0	10	1	AAF43779	Yeast NORF gene SA
117	8.4	42.0	10	1	ABV84222	Human heat shock p
c 118	8.4	42.0	10	1	ABV84641	Human HCC/chronic
c 119	8.4	42.0	10	1	ABV84947	Human multiple HCC
c 120	8.4	42.0	10	1	ABV78373	Human Th2 cell SAG
121	8.4	42.0	10	1	ABK95837	Solute Carrier Fam
122	8.4	42.0	10	1	ABK95838	Solute Carrier Fam
c 123	8.4	42.0	10	1	ABA97040	ZFP36 extension pr
c 124	8.4	42.0	10	1	ABK64054	Human BF gene alle
125	8.4	42.0	10	1	AAS19876	Oligonucleotide #5
c 126	8.4	42.0	10	1	ABK23567	Transcript tag DNA
127	8.4	42.0	10	1	ABK24232	Retinaldehyde-bind
128	8.4	42.0	10	1	AAS99275	Human F12 gene all
c 129	8.4	42.0	10	1	AAS16750	Human APOA4 ASO, p
c 130	8.4	42.0	10	1	ABL42671	Human maturation/a
131	8.4	42.0	11	1	ABV62380	Human skin EST 166
132	8.4	42.0	11	1	ABV69801	Human skin EST 758
133	8.4	42.0	11	1	AAX54916	C/EBP-beta antisen
134	8.4	42.0	11	1	AAF20485	Human C/EBP polynu
135	8.4	42.0	11	1	AAA34363	Human adenosine re
c 136	8.4	42.0	11	1	AAZ59919	COUP-TF inverted r
137	8.4	42.0	11	1	ABQ81854	Kaposi's Sarcoma S
c 138	8.4	42.0	11	1	ABV62551	Human skin EST 337
139	8.4	42.0	11	1	ABV62704	Human skin EST 490
140	8.4	42.0	11	1	ABV63037	Human skin EST 823
141	8.4	42.0	11	1	ABV65097	Human skin EST 288
142	8.4	42.0	11	1	ABV65146	Human skin EST 293
c 143	8.4	42.0	11	1	ABV65638	Human skin EST 342
144	8.4	42.0	11	1	ABV65978	Human skin EST 376
c 145	8.4	42.0	11	1	ABV66142	Human skin EST 392
c 146	8.4	42.0	11	1	ABV66964	Human skin EST 475
c 147	8.4	42.0	11	1	ABV67427	Human skin EST 521
148	8.4	42.0	11	1	ABV67547	Human skin EST 533
c 149	8.4	42.0	11	1	ABV68518	Human skin EST 630
c 150	8.4	42.0	11	1	ABV68762	Human skin EST 654
151	8.4	42.0	11	1	ABV69053	Human skin EST 683
c 152	8.4	42.0	11	1	ABV69138	Human skin EST 692
c 153	8.4	42.0	11	1	ABV69411	Human skin EST 719
c 154	8.4	42.0	11	1	ABV69528	Human skin EST 731
c 155	8.4	42.0	11	1	ABV69972	Human skin EST 775
156	8.4	42.0	11	1	ABV70125	Human skin EST 791
157	8.4	42.0	11	1	ABV70458	Human skin EST 824
158	8.4	42.0	11	1	ABQ86459	Human skin stress/
c 159	8.4	42.0	11	1	ABQ86573	Human skin stress/
160	8.4	42.0	11	1	ABQ87161	Human skin stress/
161	8.4	42.0	11	1	ABQ87207	Human skin stress/
162	8.4	42.0	11	1	ABL92021	Short human Tumour
163	8.4	42.0	11	1	ABX71946	DNA tag used to id
164	8	40.0	8	1	AAA80792	A. thaliana primer
c 165	8	40.0	9	1	AAV63091	Human Tcf mutant D
c 166	8	40.0	9	1	AAX99683	Tcf optimal respon
c 167	8	40.0	9	1	ABQ72076	Zinc finger protei
c 168	8	40.0	9	1	ABQ72078	Zinc finger protei
c 169	8	40.0	9	1	ABQ72126	Zinc finger protei
170	8	40.0	10	1	AAC73935	Human dendritic ce
171	8	40.0	10	1	ABA06204	Human normal hepat
172	8	40.0	10	1	AAH64388	Human ubiquitously
173	8	40.0	10	1	AAH64389	Human ubiquitously
174	8	40.0	10	1	AAH64390	Human ubiquitously
175	8	40.0	10	1	AAH64391	Human ubiquitously
176	8	40.0	10	1	AAH64392	Human ubiquitously
177	8	40.0	10	1	AAH64393	Human ubiquitously
178	8	40.0	10	1	AAH64394	Human ubiquitously
179	8	40.0	10	1	ABV84947	Human multiple HCC
180	8	40.0	10	1	ABV78373	Human Th2 cell SAG
181	8	40.0	10	1	ABL42671	Human maturation/a
c 182	8	40.0	10	1	AAQ51821	mdr-1 mRNA ribozym
183	8	40.0	10	1	AAQ96792	HIV-1 NL4-3 nef ge
184	8	40.0	10	1	AAQ96793	HIV-1 NL4-3 nef ge
c 185	8	40.0	10	1	AAQ88580	Human mitochondria
c 186	8	40.0	10	1	AAX54584	Human beta tryptas
c 187	8	40.0	10	1	AAX18625	p53 serial analysi
c 188	8	40.0	10	1	AAF20153	Human beta tryptas
c 189	8	40.0	10	1	AAA56555	Human macrophage g
c 190	8	40.0	10	1	AAA34031	Human adenosine re
c 191	8	40.0	10	1	AAZ77634	Human dendritic ce
c 192	8	40.0	10	1	AAZ79103	Human dendritic ce
c 193	8	40.0	10	1	AAZ79322	Human dendritic ce
c 194	8	40.0	10	1	AAZ81594	Metastatic breast
195	8	40.0	10	1	AAZ82082	Metastatic breast
196	8	40.0	10	1	AAZ83064	Metastatic breast
c 197	8	40.0	10	1	AAZ83312	Metastatic breast
c 198	8	40.0	10	1	AAZ83787	Metastatic breast
199	8	40.0	10	1	AAZ83855	Metastatic breast
200	8	40.0	10	1	AAZ83864	Metastatic breast
201	8	40.0	10	1	AAZ84284	Metastatic breast
c 202	8	40.0	10	1	AAZ85316	Metastatic breast
c 203	8	40.0	10	1	AAZ85453	Metastatic breast
c 204	8	40.0	10	1	AAZ85585	Metastatic breast
c 205	8	40.0	10	1	AAZ85596	Metastatic breast
206	8	40.0	10	1	AAZ85958	Metastatic breast
207	8	40.0	10	1	ABA06090	Human normal hepat
208	8	40.0	10	1	AAH63781	Human ubiquitously
c 209	8	40.0	10	1	AAH64036	Human ubiquitously
c 210	8	40.0	10	1	AAH64037	Human ubiquitously
c 211	8	40.0	10	1	AAH64374	Human ubiquitously
c 212	8	40.0	10	1	AAH64375	Human ubiquitously
213	8	40.0	10	1	AAH32825	LPS activated huma
c 214	8	40.0	10	1	AAH32856	LPS activated huma
c 215	8	40.0	10	1	AAF39487	Yeast NORF gene SA
c 216	8	40.0	10	1	AAF41493	Yeast NORF gene SA
217	8	40.0	10	1	ABV84307	Human chronic hepa
218	8	40.0	10	1	ABV84789	Human gamma-glutam
219	8	40.0	10	1	ABV78459	Human Th1 cell pre
220	8	40.0	10	1	ABL57664	Human SCYA24 prime
221	8	40.0	10	1	ABK95840	Solute Carrier Fam
c 222	8	40.0	10	1	ABK72637	Leukotriene B4 rec
c 223	8	40.0	10	1	ABK17015	Pyridoxal (Pyridox
224	8	40.0	10	1	AAS99416	Aldehyde dehydroge
225	8	40.0	10	1	AAS95685	Superoxide dismuta
226	8	40.0	10	1	ABL36370	Human lysosomal ac
227	8	40.0	10	1	ABL42760	Human maturation/a
c 228	8	40.0	10	1	ABL42855	Human maturation/a
229	7.8	39.0	11	1	ABQ81865	Kaposi's Sarcoma S
230	7.8	39.0	11	1	ABV64637	Human skin EST 242
231	7.8	39.0	11	1	ABV69138	Human skin EST 692
232	7.8	39.0	11	1	ABQ86573	Human skin stress/
c 233	7.8	39.0	12	1	ABZ72939	Rod opsin hammerhe
c 234	7.8	39.0	17	1	AAD03853	Human cell cycle c
c 235	7.8	39.0	17	1	AAS18424	Degenerate PCR pri
c 236	7.8	39.0	17	1	ABX16354	Human checkpoint g
237	7.6	38.0	20	1	AAX29342	Chemically modifie
c 238	7.6	38.0	20	1	AAX29331	JNK2-specific prob
c 239	7.6	38.0	20	1	AAC62874	JNK antisense olig
240	7.6	38.0	20	1	AAC62885	JNK antisense olig
c 241	7.6	38.0	20	1	AAA48651	Antisense oligonuc
c 242	7.6	38.0	20	1	AAH23754	JNK1 antisense oli
c 243	7.6	38.0	20	1	AAF99183	Immunostimulatory
c 244	7.6	38.0	20	1	ABS77827	Angiogenesis inhib
c 245	7.6	38.0	20	1	ABL39057	Immunostimulatory
c 246	7.4	37.0	9	1	AAX54706	Human fibronectin
c 247	7.4	37.0	9	1	AAF20275	Human fibronectin
c 248	7.4	37.0	9	1	AAA34153	Human adenosine re
249	7.4	37.0	9	1	ABQ71850	Zinc finger protei
250	7.4	37.0	9	1	ABQ71851	Zinc finger protei
251	7.4	37.0	10	1	AAZ82328	Metastatic breast
252	7.4	37.0	10	1	AAZ77977	Human dendritic ce

	253	7.4	37.0	10	1	AAZ84966	Metastatic breast
	254	7.4	37.0	10	1	AAH76342	Z. mays Ms45 promo
c	255	7.4	37.0	10	1	AAH76345	Z. mays Ms45 promo
	256	7.4	37.0	10	1	AAH76348	Z. mays Ms45 promo
c	257	7.4	37.0	10	1	AAS19876	Oligonucleotide #5
	258	7.4	37.0	10	1	AAH64374	Human ubiquitously
	259	7.4	37.0	10	1	AAH64375	Human ubiquitously
	260	7.4	37.0	10	1	AAH32856	LPS activated huma
c	261	7.4	37.0	10	1	ABK95840	Solute Carrier Fam
c	262	7.4	37.0	11	1	ABV65097	Human skin EST 288
	263	7.4	37.0	11	1	ABV69411	Human skin EST 719
	264	7.4	37.0	19	1	AAA82879	cdk4 ribozyme bind
	265	7.4	37.0	19	1	AAH58041	Cell-cycle depende
c	266	7	35.0	8	1	AAT09655	3'-primer used for
c	267	7	35.0	8	1	AAT09656	3'-primer used for
	268	7	35.0	8	1	AAT09366	5'-primer used for
	269	7	35.0	8	1	AAT09389	5'-primer used for
	270	7	35.0	8	1	AAT09459	5'-primer used for
c	271	7	35.0	8	1	AAT09572	3'-primer used for
c	272	7	35.0	8	1	AAX29560	Primer for human G
c	273	7	35.0	8	1	AAX29558	Primer for human G
	274	7	35.0	8	1	AAA80793	A. thaliana primer
	275	7	35.0	8	1	AAA81046	A. thaliana primer
c	276	7	35.0	8	1	AAD22387	Oligonucleotide #1
c	277	7	35.0	9	1	AAF20849	Human adenosine A1
c	278	7	35.0	9	1	AAA34727	Human adenosine re
c	279	7	35.0	9	1	ABQ72098	Zinc finger protei
c	280	7	35.0	9	1	ABQ72099	Zinc finger protei
c	281	7	35.0	10	1	ABK95837	Solute Carrier Fam
c	282	7	35.0	11	1	ABV63037	Human skin EST 823
c	283	7	35.0	11	1	ABV70458	Human skin EST 824
c	284	7	35.0	11	1	ABQ87161	Human skin stress/
	285	6.8	34.0	10	1	AAS19877	Oligonucleotide #5
	286	6.8	34.0	10	1	AAX18625	p53 serial analysi
	287	6.8	34.0	10	1	AAZ79322	Human dendritic ce
c	288	6.8	34.0	10	1	AAZ83064	Metastatic breast
c	289	6.8	34.0	10	1	AAZ83855	Metastatic breast
	290	6.8	34.0	10	1	AAZ85316	Metastatic breast
	291	6.8	34.0	10	1	AAH64036	Human ubiquitously
	292	6.8	34.0	10	1	AAH64037	Human ubiquitously
	293	6.8	34.0	11	1	AAX55034	C/EBP-beta antisen
	294	6.8	34.0	11	1	AAF20603	Human C/EBP polynu
	295	6.8	34.0	11	1	AAA34481	Human adenosine re
	296	6.8	34.0	11	1	ABV68762	Human skin EST 654
	297	6.8	34.0	12	1	AAX55033	C/EBP-beta antisen
	298	6.8	34.0	12	1	AAF20602	Human C/EBP polynu
	299	6.8	34.0	12	1	AAA34480	Human adenosine re
	300	6.4	32.0	8	1	AAX29560	Primer for human G

ALIGNMENTS

RESULT 1
AAX29342/c
ID AAX29342 standard; DNA; 20 BP.
XX
AC AAX29342;
XX
DT 10-JUN-1999 (first entry)
XX
DE Chemically modified sense control probe ISIS No: 14318.
XX
KW Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KW hyperproliferative disease; human; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9909214-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-US16488.
XX
PR 13-AUG-1997; 97US-0910629.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean N, Gaarde WA, Mckay R, Monia BP, Nero PS;
XX
DR WPI; 1999-181060/15.
XX
PT New antisense oligonucleotides that detect and modulate the
PT expression of Jun N-terminal kinase proteins - useful for treating
PT hyperproliferative diseases and inhibiting tumor growth in animals,
PT and for modulating protein phosphorylation by these proteins
XX
PS Example 4; Page 92; 190pp; English.
XX
CC The invention relates to antisense oligonucleotides that detect and
CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal.
XX
SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCCAAAGTC 20
||||||||||||||||||||
Db 20 GTCCGGGCCAGGCCAAAGTC 1

RESULT 2
AAX29331
ID AAX29331 standard; DNA; 20 BP.
XX
AC AAX29331;
XX
DT 10-JUN-1999 (first entry)
XX
DE JNK2-specific probe ISIS No: 12560.
XX
KW Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KW hyperproliferative disease; human; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9909214-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-US16488.
XX
PR 13-AUG-1997; 97US-0910629.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean N, Gaarde WA, Mckay R, Monia BP, Nero PS;
XX
DR WPI; 1999-181060/15.
XX

```
PT   New antisense oligonucleotides that detect and modulate the
PT   expression of Jun N-terminal kinase proteins  - useful for treating
PT   hyperproliferative diseases and inhibiting tumor growth in animals,
PT   and for modulating protein phosphorylation by these proteins
XX
PS   Example 4; Page 87; 190pp; English.
XX
CC   The invention relates to antisense oligonucleotides that detect and
CC   modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC   oligonucleotides specifically hybridize to a nucleic acid encoding a
CC   JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC   proteins. The oligonucleotides are useful for modulating JNK protein
CC   expression and cell cycle progression in cultured cells or animal cells.
CC   The oligonucleotides are also useful for modulating the phosphorylation
CC   of a protein that has been phosphorylated by a JNK protein, and the
CC   expression of a cellular protein that promotes one or more metastatic
CC   events. The oligonucleotides also form pharmaceutical compositions for
CC   treating animals with a hyperproliferative disease, and for inhibiting
CC   tumor growth in an animal.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 3
AAC62874
ID   AAC62874 standard; DNA; 20 BP.
XX
AC   AAC62874;
XX
DT   06-FEB-2001  (first entry)
XX
DE   JNK antisense oligonucleotide ISIS #12560.
XX
KW   Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
KW   cellular hyperproliferation; Alzheimer's; Parkinson's disease;
KW   amylotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
KW   myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
KW   diabetes; Jun N-terminal kinase; ss.
XX
OS   Homo sapiens.
XX
PN   WO200059549-A1.
XX
PD   12-OCT-2000.
XX
PF   04-APR-2000; 2000WO-US08880.
XX
PR   07-APR-1999;   99US-0287796.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Mckay R,  Dean NM,  Monia BP,  Nero PS,  Gaarde WA;
XX
DR   WPI; 2000-638427/61.
XX
PT   Novel methods for reducing apoptosis comprising contacting cells with
PT   antisense oligonucleotides, useful for treating apoptotic disorders,
PT   e.g. cancer -
XX
PS   Claim 3; Page 133; 160pp; English.
XX
CC   The present invention relates to antisense oligonucleotides
CC   (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC   specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC   protein, resulting in decrease of JNK2 expression and leading to
CC   induction of apoptosis. The present sequence is one such antisense
CC   oligonucleotide. The oligonucleotides of the present invention are useful
CC   for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC   and cellular hyperproliferation. The oligonucleotides may also be used to
CC   increase the stimulation of apoptotic proteins, e.g. for treating
CC   Alzheimer's or Parkinson's disease, amylotrophic lateral sclerosis,
CC   retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC   obstructive jaundice, polycystic kidney and diabetes. The present
CC   sequence may have a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 4
AAC62885/c
ID   AAC62885 standard; DNA; 20 BP.
XX
AC   AAC62885;
XX
DT   06-FEB-2001  (first entry)
XX
DE   JNK antisense oligonucleotide ISIS #14318.
XX
KW   Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
KW   cellular hyperproliferation; Alzheimer's; Parkinson's disease;
KW   amylotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
KW   myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
KW   diabetes; Jun N-terminal kinase; ss.
XX
OS   Homo sapiens.
XX
PN   WO200059549-A1.
XX
PD   12-OCT-2000.
XX
PF   04-APR-2000; 2000WO-US08880.
XX
PR   07-APR-1999;   99US-0287796.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Mckay R,  Dean NM,  Monia BP,  Nero PS,  Gaarde WA;
XX
DR   WPI; 2000-638427/61.
XX
PT   Novel methods for reducing apoptosis comprising contacting cells with
PT   antisense oligonucleotides, useful for treating apoptotic disorders,
PT   e.g. cancer -
XX
PS   Example 4; Page 135; 160pp; English.
XX
CC   The present invention relates to antisense oligonucleotides
CC   (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC   specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC   protein, resulting in decrease of JNK2 expression and leading to
CC   induction of apoptosis. The present sequence is one such antisense
CC   oligonucleotide. The oligonucleotides of the present invention are useful
CC   for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC   and cellular hyperproliferation. The oligonucleotides may also be used to
CC   increase the stimulation of apoptotic proteins, e.g. for treating
CC   Alzheimer's or Parkinson's disease, amylotrophic lateral sclerosis,
CC   retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC   obstructive jaundice, polycystic kidney and diabetes. The present
CC   sequence may have a phosphorothioate backbone.
XX
```

```
SQ   Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;

  Query Match          100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db         20 GTCCGGGCCAGGCCAAAGTC 1


RESULT 5
AAA48651
ID   AAA48651 standard; DNA; 20 BP.
XX
AC   AAA48651;
XX
DT   20-SEP-2000  (first entry)
XX
DE   Antisense oligonucleotide ISIS no.15354 to human JNK2 gene.
XX
KW   Antisense; E-selectin; TNF alpha; cell adhesion;
KW   tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;
KW   sepsis; rheumatoid arthritis; inflammatory; immune disease;
KW   inflammatory bowel disease; allergic contact dermatitis; psoriasis;
KW   diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
KW   immunosuppressive; antipsoriatic; antidiabetic; antithyroid;
KW   cytostatic; dermatological; antiallergic; Ha-ras; c-raf;
KW   c-Jun N-terminal kinase; JNK; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "All bases are 2'-methoxyethoxy,
FT                   additionally C bases are m5c"
FT   modified_base   7..15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   modified_base   16..20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "All bases are 2'-methoxyethoxy,
FT                   additionally C bases are m5c"
XX
PN   WO200034303-A1.
XX
PD   15-JUN-2000.
XX
PF   08-DEC-1999;   99WO-US28965.
XX
PR   10-DEC-1998;   98US-0209668.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Xu XS;
XX
DR   WPI; 2000-423367/36.
XX
PT   Modulating cell adhesion molecule expression for treating immune or
PT   inflammatory diseases involves treating cell with specific inhibitor of
PT   Tumour Necrosis Factor alpha signalling molecule  -
XX
PS   Claim 36; Page 46; 100pp; English.
XX
CC   A novel method for modulating cell adhesion molecule expression
CC   involves antisense inhibition of a tumour necrosis factor (TNF) alpha
CC   signalling molecule. In the method TNF alpha signalling molecules
CC   Ha-ras, c-raf and c-Jun N-terminal kinase (JNK)2 were inhibited by
CC   antisense oligonucleotides. In addition an antisense oligonucleotide
CC   to the cell adhesion molecule E-selectin was also examined. The
CC   present sequence is the JNK2 antisense oligonucleotide. The
CC   antisense oligonucleotides used in the method contained modifications,
CC   namely phosphorothioate linkages and 2'methoxyethoxy bases. Some C
CC   residues also had a 5'methyl modification. Inhibitors of the TNF alpha
CC   signalling molecules have antibacterial, immunosuppressive,
CC   antipsoriatic, antidiabetic, antithyroid, cytostatic, dermatological,
CC   antiallergic and antiinflammatory activity. The antisense inhibitors
CC   may be useful for the treatment of sepsis, rheumatoid arthritis,
CC   inflammatory, immune disease, inflammatory bowel disease, allergic
CC   contact dermatitis, psoriasis, diabetes, Grave's disease, allograft
CC   rejection and cancer.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match          100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 6
AAH23754
ID   AAH23754 standard; DNA; 20 BP.
XX
AC   AAH23754;
XX
DT   13-AUG-2001  (first entry)
XX
DE   JNK1 antisense oligonucleotide, JNK2AS, (ISIS #12560).
XX
KW   JNK; jun kinase; antisense; cytostatic; cancer;
KW   2'-O-methoxyethyl oligonucleotide; MOE; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /mod_base= "OTHER"
FT                   /note= "This oligonucleotide is a 2'-O-methoxyethyl (MOE)
FT                   chimeric antisense oligonucleotide containing five
FT                   MOE/phoshopdiester residues flanking a
FT                   2'-deoxynucleotide/phosphorothioate region"
XX
PN   WO200134792-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US30869.
XX
PR   12-NOV-1999;   99US-0165224.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Potapova O,  Gorospe M,  Holbrook NJ;
XX
DR   WPI; 2001-335925/35.
XX
PT   Use of Jun Kinase antisense mRNA for treating cancer by administering
PT   vector comprising promoter operably linked to DNA sequence that encodes
PT   the antisense mRNA to patient diagnosed with cancer  -
XX
PS   Claim 1; Page 41; 75pp; English.
XX
CC   The present invention relates to the use of Jun Kinase (JNK) antisense
CC   oligonucleotides for treating cancer and for screening compounds that
CC   mimic or augment the effect of JNK antisense oligonucleotides treatment
CC   for cancer. The present sequence is one such JNK antisense
CC   oligonucleotide.
```

```
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 7
AAF99183
ID   AAF99183 standard; DNA; 20 BP.
XX
AC   AAF99183;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #299.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US26383.
XX
PR   25-SEP-1999;   99US-0156113.
PR   27-SEP-1999;   99US-0156135.
PR   23-AUG-2000; 2000US-0227436.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids -
XX
PS   Claim 101; Page 44; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells.
CC   Note: the present sequence may have a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 8
ABS77827
ID   ABS77827 standard; DNA; 20 BP.
XX
AC   ABS77827;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #311.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis;
KW   psoriasis; diabetic retinopathy; retinopathy of prematurity;
KW   macular degeneration; corneal graft rejection; neovascular glaucoma;
KW   retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;
KW   myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW   haemophiliac joint; angiofibroma; wound granulation;
KW   intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US48458.
XX
PR   14-DEC-2000; 2000US-255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least
PT   one antiangiogenic nucleic acid molecule to the subject  -
XX
PS   Claim 2; Page 25; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule.
CC   Also included is a kit comprising a first container housing the
CC   antiangiogenic nucleic acids, and instructions for administering them to
CC   a subject having a condition characterised by unwanted angiogenesis.
CC   The method is useful for inhibiting angiogenesis associated with solid
CC   tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC   arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC   macular degeneration, corneal graft rejection, neovascular glaucoma,
CC   retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial
CC   angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
CC   joints, angiofibroma, wound granulation, intestinal adhesions,
CC   atherosclerosis, scleroderma and hypertrophic scars. The present
CC   sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 9
ABL39057
ID   ABL39057 standard; DNA; 20 BP.
```

```
XX
AC   ABL39057;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 463.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US20154.
XX
PR   22-JUN-2000; 2000US-213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer -
XX
PS   Disclosure; Page 212; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC   non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in
CC   the exemplification of the invention.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 10
AAV60744
ID   AAV60744 standard; DNA; 18 BP.
XX
AC   AAV60744;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Primer #2 for human CDK4 codons 1-163.
XX
KW   PCR primer; amplification; yeast; UAS; upstream activating sequence;
KW   transcription terminator; cell cycle; Upstream Activation Sequence; UAS;
KW   promoter; phosphorylation; cyclin; cyclin-dependent kinase; CDK; vector;
KW   cyclin kinase inhibitor; CKI; growth; wound healing; cancer therapy; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9816660-A1.
XX
PD   23-APR-1998.
XX
PF   16-OCT-1997;   97WO-US18608.
XX
PR   27-NOV-1996;   96US-0031968.
PR   16-OCT-1996;   96US-0029127.
XX
PA   (BITT-) BITTECH INC.
XX
PI   Bitter GA;
XX
DR   WPI; 1998-251302/22.
XX
PT   Screening for agents that effect cell cycle regulatory proteins -
PT   using a cell line that expresses a reporter gene in response to
PT   regulation through phosphorylation by a cyclin/CDK system
XX
PS   Example 4; Page 75; 93pp; English.
XX
CC   Primers AAV60743-V60745 were used to PCR amplify codons 1-163 of the
CC   human cyclin-dependent kinase 4 (hCDK4). The amplified product was used
CC   to generate a fusion protein comprising part of the hCDK4 sequence
CC   linked to codons 154-302 of the yeast PHO85 gene.  The fusion protein is
CC   used to screen for compounds that affect mammalian cell cycle regulatory
CC   proteins.  The method comprises administering a compound to a cell line,
CC   which contains a reporter gene linked to an Upstream Activation Sequence
CC   (UAS) and a promoter, where the UAS binds a transcription control factor
CC   (TCF) which is regulated through cyclin/cyclin-dependent kinase (CDK)
CC   phosphorylation.  Also included in the construct is an effector gene
CC   providing a gene product to permit normal cyclin/CDK regulation of the
CC   TCF.  Expression of the reporter gene is then analysed in the cell line,
CC   thereby determining whether the compound affects the normal regulation.
CC   The method can be used to identify inhibitors and activators of
CC   mammalian cell cycle regulatory proteins, especially inhibitors and
CC   activators of cyclins, CDKs, cyclin/CDK complexes, cyclin kinase
CC   inhibitors (CKIs), and cyclin/CDK/CKI complexes.  The identified agents
CC   can be used for stimulating growth of cells (as in wound healing), or
CC   regulating excessive cell growth and division (as in cancer therapy).
XX
SQ   Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 other;

  Query Match             77.0%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 10;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCCAAAGTC 20
              | ||||||||||||||||
Db          2 CTGGCCAGGCCAAAGTC 18


RESULT 11
AAA82879/c
ID   AAA82879 standard; DNA; 19 BP.
XX
AC   AAA82879;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk4 ribozyme binding site #60.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
```

KW restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-0110954.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1 -
XX
PS Disclosure; Page 53; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
CC efficient in restenosis treatment.
XX
SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;

Query Match 75.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCAAAGTC 20
||||||||||||||||
Db 19 GGCCAGGCCAAAGTC 5

RESULT 12
AAH58041/c
ID AAH58041 standard; DNA; 19 BP.
XX
AC AAH58041;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:465.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29500.
XX
PR 26-OCT-1999; 99US-0161532.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using
PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT matrix metalloproteinases, growth factors and cell-cycle dependent
PT kinases -
XX
PS Example 1; Page 105; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative
CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;

Query Match 75.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCAAAGTC 20
||||||||||||||||
Db 19 GGCCAGGCCAAAGTC 5

RESULT 13
AAX73494/c
ID AAX73494 standard; RNA; 18 BP.
XX
AC AAX73494;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hairpin ribozyme substrate #41.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.

```
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 152; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 18 BP; 1 A; 6 C; 7 G; 4 U; 0 other;

  Query Match           74.0%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity  88.9%;  Pred. No. 14;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAGTC 20
              |||||||| ||| |||||
Db         18 CCGGGCCAAGCCGAAGTC 1


RESULT 14
AAX71472/c
ID   AAX71472 standard; RNA; 17 BP.
XX
AC   AAX71472;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human KDR VEGF receptor hammerhead ribozyme substrate #484.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 111; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 0 A; 5 C; 7 G; 5 U; 0 other;

  Query Match           72.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity  93.8%;  Pred. No. 15;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              |||||||| |||||||
Db         16 CCGGGCCAAGCCAAAG 1


RESULT 15
AAX74911/c
ID   AAX74911 standard; RNA; 17 BP.
XX
AC   AAX74911;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #439.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Mus sp.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 168; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
```

```
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 1 A; 5 C; 6 G; 5 U; 0 other;

  Query Match             70.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAAAGTC 20
              ||||||||||||||
Db         17 GCCAGGCCAAAGTC 4


RESULT 16
AAX69246/c
ID   AAX69246 standard; RNA; 17 BP.
XX
AC   AAX69246;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #541.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 63; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 1 A; 5 C; 6 G; 5 U; 0 other;

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 25;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAA 17
              |||||| ||||||||
Db         15 CCGGGCAAGGCCAAA 1


RESULT 17
AAD03853
ID   AAD03853 standard; DNA; 17 BP.
XX
AC   AAD03853;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Human cell cycle checkpoint protein, hchk1 DNA amplifying PCR primer #2.
XX
KW   Human; cell cycle checkpoint; chk1; tumour; malignancy;
KW   cell growth inhibitor; development deficiency; PCR primer;
KW   DNA damage; kinase; ss.
XX
OS   Homo sapiens.
XX
PN   US6218109-B1.
XX
PD   17-APR-2001.
XX
PF   05-SEP-1997;   97US-0924183.
XX
PR   05-SEP-1997;   97US-0924183.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Elledge SJ,  Sanchez Y;
XX
DR   WPI; 2001-289827/30.
XX
PT   New Chk1 proteins and gene sequences encoding the proteins useful as
PT   probes for a portion of the chromosome associated with tumors and other
PT   malignancies, growth and/or development deficiencies  -
XX
PS   Claim 17; Column 24; 37pp; English.
XX
CC   The present sequence is a degenerate PCR primer used for amplifying the
CC   human cell cycle checkpoint protein, hchk1 DNA. The cell cycle
CC   checkpoints are regulatory pathways that control the order and timing of
CC   cell cycle transitions, and ensure that critical events such as DNA
CC   replication and chromosome segregation are completed with high fidelity.
CC   The chk1 protein controls cell cycle in response to DNA damage. It
CC   functions as kinase and phosphorylates the key regulators of Cdk tyrosine
CC   phosphorylation. The checkpoint gene sequences are used as probes for a
CC   portion of the chromosome associated with tumours and other malignancies,
CC   as well as growth and/or development deficiencies. The chk1 proteins are
CC   useful for generating specific antibodies and for inhibiting growth of
CC   cells.
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 25;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              || ||||||||||||
Db          3 GGACAGGCCAAAGTC 17


RESULT 18
AAS18424
ID   AAS18424 standard; DNA; 17 BP.
XX
AC   AAS18424;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Degenerate PCR primer #2 used to amplify DNA encoding human chk1.
XX
```

KW Human; checkpoint protein; hchk1; DNA damage; chromosome 11q24;
KW cell cycle checkpoint pathway; inhibition of cell growth; tumour;
KW malignancy; growth deficiency; development deficiency; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6307015-B1.
XX
PD 23-OCT-2001.
XX
PF 12-JAN-2000; 2000US-0488364.
XX
PR 05-SEP-1997; 97US-0924183.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Elledge SJ, Sanchez Y;
XX
DR WPI; 2002-040207/05.
XX
PT New mammalian checkpoint protein and gene, for generating specific
PT antibodies or for inhibiting the growth of cells, and for use as a
PT probe for a portion of a chromosome associated with tumours or
PT malignancies -
XX
PS Example 1; Column 24; 39pp; English.
XX
CC The present invention relates to the isolation of human and mouse
CC checkpoint (chk1) proteins and the nucleic acid sequences encoding them.
CC Human chk1 (hchk1) maps to chromosome 11q24. Chk1 is involved in
CC cellular responses to DNA damage, in the cell cycle checkpoint pathway.
CC The protein is useful for generating specific antibodies and for
CC inhibiting the growth of cells. The nucleotide sequence encoding the
CC protein may be used as a probe for a portion of the chromosome
CC associated with tumours and other malignancies, as well as growth and/or
CC development deficiencies. The present sequence represents a degenerate
CC PCR primer used to amplify DNA encoding human chk1 protein.
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCAAAGTC 20
|| |||||||||||
Db 3 GGACAGGCCAAAGTC 17

RESULT 19
ABX16354
ID ABX16354 standard; DNA; 17 BP.
XX
AC ABX16354;
XX
DT 08-APR-2003 (first entry)
XX
DE Human checkpoint gene Chk1 PCR primer #2.
XX
KW Human; checkpoint; chk1; anti-Chk1 antibody; tumour;
KW PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002156247-A1.
XX
PD 24-OCT-2002.
XX
PF 12-DEC-2001; 2001US-0020038.
XX
PR 12-JAN-2000; 2000US-0488364.
XX
PA (ELLE/) ELLEDGE S J.
PA (SANC/) SANCHEZ Y.
XX
PI Elledge SJ, Sanchez Y;
XX
DR WPI; 2003-182651/18.
XX
PT New anti-Chk1 antibody, that may be a monoclonal or polyclonal
PT antibody, useful for detecting a Chk1 protein that is associated with a
PT tumor -
XX
PS Example 1; Page 13; 28pp; English.
XX
CC The invention describes an anti-Chk1 antibody capable of specifically
CC binding to an antigenic determinant on the proteins encoded by a
CC sequence comprising 476 (3 sequences), 479, 496 or 513 amino acids.
CC A new method is used to produce the antibody, which is useful for
CC detecting a Chk1 protein that is associated with a tumour. This
CC sequence represents a PCR primer used to isolate DNA encoding the
CC human checkpoint protein Chk1.
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCAAAGTC 20
|| |||||||||||
Db 3 GGACAGGCCAAAGTC 17

RESULT 20
AAX74910/c
ID AAX74910 standard; RNA; 17 BP.
XX
AC AAX74910;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #438.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 4; Page 168; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more

```
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 1 A; 4 C; 6 G; 6 U; 0 other;

  Query Match            65.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAAGTC 20
              |||||||||||||
Db         17 CCAGGCCAAAGTC 5


RESULT 21
AAX73045/c
ID   AAX73045 standard; RNA; 17 BP.
XX
AC   AAX73045;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #478.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Mus sp.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 138; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 0 A; 6 C; 7 G; 4 U; 0 other;

  Query Match            64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity  87.5%;  Pred. No. 35;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              |||||||| ||| |||
Db         16 CCGGGCCAAGCCGAAG 1


RESULT 22
AAS19798
ID   AAS19798 standard; DNA; 15 BP.
XX
AC   AAS19798;
XX
DT   08-MAY-2002  (first entry)
XX
DE   ASO primer #56 to detect human RANGAP1 gene polymorphisms.
XX
KW   Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KW   chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW   cancer; irregular cell cycle associated disorder; ASO; primer; ss;
KW   allele-specific oligonucleotide.
XX
OS   Homo sapiens.
XX
PN   WO200179240-A2.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-US12455.
XX
PR   17-APR-2000; 2000US-198072P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-075068/10.
XX
PT   Genotyping human Ran GTPase activating protein 1 gene of individual for
PT   determining haplotype of individual, involves determining identity of
PT   nucleotide pair at specific polymorphic sites for two copies of the
PT   gene  -
XX
PS   Claim 15; Page 15; 148pp; English.
XX
CC   The present invention relates to novel single nucleotide polymorphisms
CC   (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC   located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC   genotyping the RANGAP1 gene. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC   primer-extension oligonucleotides for detecting the RANGAP1 gene
CC   polymorphisms. The polynucleotides and screened compounds are useful for
CC   treatment of diseases associated with RANGAP1 activity, such as
CC   cancer and other disorders associated with an irregular cell cycle.
CC   AAS19743-AAS19820 represent ASO primers for detecting human RANGAP1
CC   gene polymorphisms.
XX
SQ   Sequence 15 BP; 3 A; 6 C; 5 G; 0 U; 1 other;

  Query Match            57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity  92.3%;  Pred. No. 52;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCA 15
              |||||||||| ||
Db          1 CCGGGCCAGGACA 13


RESULT 23
AAT76461/c
ID   AAT76461 standard; DNA; 14 BP.
```

```
XX
AC   AAT76461;
XX
DT   16-SEP-1997  (first entry)
XX
DE   Chymase antisense oligonucleotide.
XX
KW   Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW   chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS   Synthetic.
XX
PN   WO9640162-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US09306.
XX
PR   07-JUN-1995;   95US-0474497.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Metzger WJ,  Nyce JW;
XX
DR   WPI; 1997-051871/05.
XX
PT   Treatment of airway diseases such as asthma - by topically applying
PT   adenosine-free antisense oligo:nucleotide to airway epithelium of
PT   subject
XX
PS   Example 5; Page 41; 71pp; English.
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide specific
CC   for chymase. The method can be used to treat airway diseases such as
CC   cystic fibrosis, asthma, chronic obstructive pulmonary disease,
CC   bronchitis and other airway diseases characterised by an inflammatory
CC   response. By eliminating adenosine from the antisense ON, its liberation
CC   upon antisense degradation is prevented, thereby preventing adenosine-
CC   induced bronchoconstriction in patients with hyper-reactive airways.
XX
SQ   Sequence 14 BP; 0 A; 8 C; 3 G; 3 T; 0 other;

  Query Match           54.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity  85.7%;  Pred. No. 59;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCCAAAG 18
              |||||||| ||| |
Db         14 GGGCCAGGGCAAGG 1


RESULT 24
AAX54253/c
ID   AAX54253 standard; DNA; 14 BP.
XX
AC   AAX54253;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Chymase antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 60; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 14 BP; 0 A; 8 C; 3 G; 3 T; 0 other;

  Query Match           54.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity  85.7%;  Pred. No. 59;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCCAAAG 18
              |||||||| ||| |
Db         14 GGGCCAGGGCAAGG 1


RESULT 25
AAF19819/c
ID   AAF19819 standard; DNA; 14 BP.
XX
AC   AAF19819;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human chymase polynucleotide fragment #1386.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
```

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 250; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 14 BP; 0 A; 8 C; 3 G; 3 T; 0 other;

Query Match 54.0%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGGCCAGGCCAAAG 18
||||||| ||| |
Db 14 GGGCCAGGGCAAGG 1

RESULT 26
AAA33697/c
ID AAA33697 standard; DNA; 14 BP.
XX
AC AAA33697;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:1386.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Claim 18; Page 438; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 14 BP; 0 A; 8 C; 3 G; 3 T; 0 other;

Query Match 54.0%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGGCCAGGCCAAAG 18
||||||| ||| |
Db 14 GGGCCAGGGCAAGG 1

```
RESULT 27
AAZ41523
ID   AAZ41523 standard; DNA; 12 BP.
XX
AC   AAZ41523;
XX
DT   19-JAN-2000  (first entry)
XX
DE   Microbe detection in organic waste arbitrarily primed PCR primer #100.
XX
KW   Microbe; detection; organic waste; arbitrarily primer PCR;
KW   random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP11276176-A.
XX
PD   12-OCT-1999.
XX
PF   31-MAR-1998;   98JP-0087652.
XX
PR   31-MAR-1998;   98JP-0087652.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR   WPI; 1999-626940/54.
XX
PT   Amplification of a DNA fragment - in order to establish the state of
PT   existence of a microbe
XX
PS   Claim 1; Page 9; 40pp; Japanese.
XX
CC   A method has been developed for the amplification of a DNA fragment in
CC   which amplification is carried out on the DNA fragments of a number of
CC   different DNAs. The method comprises a PCR reaction repeatedly carrying
CC   out a heat-denaturing step, a primer annealing step and a polymerase
CC   extending step, to amplify the DNA fragments of a plural of different
CC   DNAs. The method can detect the existence of a microbe in organic waste.
CC   AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC   polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC   organic waste.
XX
SQ   Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 50;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 28
AAZ41739
ID   AAZ41739 standard; DNA; 12 BP.
XX
AC   AAZ41739;
XX
DT   20-MAR-2003  (updated)
DT   21-JAN-2000  (first entry)
XX
DE   Organic material detecting primer 100.
XX
KW   Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW   detection; pollutant; soil; food; agricultural chemical; polymer;
KW   organochlorine; primer; ss.
XX
OS   Synthetic.
XX
PN   DE19914461-A1.
XX
PD   21-OCT-1999.
XX
PF   30-MAR-1999;   99DE-1014461.
XX
PR   31-MAR-1998;   98JP-0087651.
PR   16-MAR-1999;   99JP-0069694.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI   Inoue T;
XX
DR   WPI; 1999-592157/51.
XX
PT   Novel polymerase chain reaction method, for differentiating between
PT   microorganisms and for detecting contaminants -
XX
PS   Example 1; Page 19; 78pp; German.
XX
CC   This invention describes a novel method for the amplification of DNA
CC   comprising (i) preparing many primers (P) with different probabilities
CC   of amplification and (ii) simultaneous polymerase chain reaction (PCR)
CC   of many different DNA using these primers. The method is used (i) to
CC   differentiate between different microorganisms in a mixed population
CC   and (ii) to determine presence/absence of an impurity (pollutant), or
CC   its concentration, in e.g. soil, foods, compost etc., typically metals,
CC   agricultural chemicals, polymers, organochlorine compounds etc. A
CC   particular use is monitoring composting of organic material.
CC   Amplification with many primers produces a lot of information, so
CC   reliability of the test is improved, and many samples may be tested
CC   quickly. AAZ41640-Z41855 represent the primers described in the method
CC   of the invention.
CC   (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 50;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 29
AAC97874
ID   AAC97874 standard; DNA; 12 BP.
XX
AC   AAC97874;
XX
DT   28-FEB-2001  (first entry)
XX
DE   Primer used to illustrate DNA amplification method SEQ ID 100.
XX
KW   Primer; amplification; selective; ss.
XX
OS   Synthetic.
XX
PN   JP2000270867-A.
XX
PD   03-OCT-2000.
XX
PF   19-MAR-1999;   99JP-0076844.
XX
PR   19-MAR-1999;   99JP-0076844.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR   WPI; 2001-011047/02.
XX
```

```
PT   Amplification of a DNA fragment and its apparatus  -
XX
PS   Example 1; Page 9; 32pp; Japanese.
XX
CC   This invention relates to a method for amplifying a DNA fragment. The
CC   method comprises successive repetitions of heat-denaturing, annealing of
CC   a primer and an extending step using a DNA polymerase. The method makes
CC   use of a cDNA pool in which the primer is one primer or a pair of primer
CC   sets and has an amplification probability which allows it to amplify a
CC   DNA fragment from a limited number of the cDNAs among the DNA pool
CC   (where the limited number is in the range of 1 to 25). Also included in
CC   the invention are apparatus used for carrying out the method, a primer
CC   and a DNA polymerase and a kit used for amplifying a DNA fragment. The
CC   method can be used to amplify a limited number of cDNAs from a pool in
CC   which a wide variety of cDNAs are present. Oligonucleotides AAC97775 -
CC   AAC97990 represent primers used in an example illustrating the method of
CC   the invention.
XX
SQ   Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 50;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 30
AAZ81584/c
ID   AAZ81584 standard; DNA; 10 BP.
XX
AC   AAZ81584;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #818.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 80; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||||||||||
Db         10 TCCGGGCCAG 1


RESULT 31
AAZ86676/c
ID   AAZ86676 standard; DNA; 10 BP.
XX
AC   AAZ86676;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5910.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 214; 219pp; English.
XX
```

```
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||||||||||
Db         10 GCCAGGCCAA 1


RESULT 32
AAH64570/c
ID   AAH64570 standard; cDNA; 10 BP.
XX
AC   AAH64570;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1410.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 71; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||||||||||
Db         10 TCCGGGCCAG 1


RESULT 33
AAH64571/c
ID   AAH64571 standard; cDNA; 10 BP.
XX
AC   AAH64571;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1411.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 71; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||||||||||
Db         10 TCCGGGCCAG 1


RESULT 34
ABZ72939
ID   ABZ72939 standard; RNA; 12 BP.
```

```
XX
AC   ABZ72939;
XX
DT   09-APR-2003  (first entry)
XX
DE   Rod opsin hammerhead ribozyme oligonucleotide.
XX
KW   Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease;
KW   target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW   diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW   blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200288320-A2.
XX
PD   07-NOV-2002.
XX
PF   01-MAY-2002; 2002WO-US13679.
XX
PR   01-MAY-2001; 2001US-0847601.
XX
PA   (UYFL ) UNIV FLORIDA.
XX
PI   Lewin AS,  Shaw LC,  Grant MB;
XX
DR   WPI; 2003-111880/10.
XX
PT   A recombinant adeno-associated virus-vectored ribozyme composition,
PT   useful for treating a disease or dysfunction of the mammalian eye e.g.
PT   retinal disease, e.g. diabetic retinopathy or age-related macular
PT   degeneration -
XX
PS   Example 5; Page 73; 115pp; English.
XX
CC   The present invention describes a recombinant adeno-associated virus
CC   (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC   first ribozyme that specifically cleaves an mRNA encoding a protein,
CC   polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC   RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC   alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC   vector comprising a polynucleotide encoding the ribozyme, where the
CC   polynucleotide operably positioned downstream of at least a first
CC   promoter that directs expression of the polynucleotide in a selected
CC   mammalian cell transformed with the vector; (c) a viral particle
CC   comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC   comprising the ribozyme or the polynucleotide; or (e) a host cell
CC   comprising the ribozyme or the polynucleotide. Also described is a method
CC   for decreasing the amount of mRNA encoding a selected polypeptide in a
CC   retinal cell of a mammalian eye, comprising providing to the eye the
CC   composition described above, and for a time effective to specifically
CC   cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC   be used in gene therapy. (I) can be used for treating a disease or
CC   dysfunction of the mammalian eye, such as a retinal disease or retinal
CC   dysfunction, (diabetic) retinopathy, or (age-related) macular
CC   degeneration. (I) is also useful for manufacturing a medicament for
CC   treating the diseases mentioned above, including autosomal dominant
CC   retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC   for treating, decreasing the severity, or ameliorating the symptoms of a
CC   pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC   blindness, a reduction in central or peripheral vision, or a reduction in
CC   total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 12 BP; 3 A; 4 C; 4 G; 1 U; 0 other;

  Query Match            50.0%;  Score 10;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 61;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              ||||||||||
Db          3 GGCCAGGCCA 12


RESULT 35
AAV63772/c
ID   AAV63772 standard; DNA; 13 BP.
XX
AC   AAV63772;
XX
DT   26-APR-1999  (first entry)
XX
DE   Human JAGGED1 exon 23 mutation associated with Alagille Syndrome.
XX
KW   JAGGED; JAGGED1; hJAGGED1; human; notch ligand; stem cell;
KW   progenitor cell; haematopoiesis; cell differentiation; mutant;
KW   Alagille syndrome; leukaemia; lymphoma; diagnosis; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mutation        7..11
FT                   /*tag=  a
FT                   /note= "5-base insertion"
XX
PN   WO9858958-A2.
XX
PD   30-DEC-1998.
XX
PF   25-JUN-1998;   98WO-US13207.
XX
PR   25-JUN-1997;   97US-0882046.
XX
PA   (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Hood L,  Krantz ID,  Li L,  Spinner NB;
XX
DR   WPI; 1999-081220/07.
XX
PT   New Jagged peptides for inhibiting differentiation of progenitor
PT   cells - also used for maintaining these cells in undifferentiated
PT   state, e.g. for haematopoietic reconstitution
XX
PS   Example 5; Fig 8; 101pp; English.
XX
CC   This nucleotide corresponds to a portion of exon 23 of the human
CC   JAGGED1 gene that is mutated in affected individuals of an
CC   Alagille Syndrome (AS) family.  The mutation involves insertion of
CC   'GTGGC' residues at a position corresponding to nucleotide 3102
CC   (see AAV63773) of an hJAGGED1 cDNA (see AAV63753).  The mutation causes
CC   a frameshift that results in premature truncation of the gene
CC   product (see AAW87904).  It was detected by heteroduplex mobility
CC   analysis (see AAV63767-68 and AAV84310-19).  hJAGGED1 (see also
CC   AAW87894) is a novel Notch ligand capable of inhibiting the
CC   differentiation of haematopoietic progenitor cells.  Methods are provided
CC   for the diagnosis of AS based on detection of disease-associated
CC   mutations or truncated hJAGGED1 gene products.
XX
SQ   Sequence 13 BP; 0 A; 4 C; 6 G; 3 T; 0 other;

  Query Match            49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  84.6%;  Pred. No. 81;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCCAAA 17
              |||||| |||| |
Db         13 GGGCCACGCCACA 1


RESULT 36
AAA04950/c
ID   AAA04950 standard; DNA; 13 BP.
XX
```

```
AC   AAA04950;
XX
DT   18-MAY-2000  (first entry)
XX
DE   Tenascin-C phosphorothioate antisense oligonucleotide SEQ ID NO:239.
XX
KW   Human; Tenascin-C; extracellular matrix protein; phosphorothioate;
KW   antisense oligonucleotide; inhibition; exon deletion; therapy;
KW   cellular development; differentiation; translation; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200006775-A1.
XX
PD   10-FEB-2000.
XX
PF   23-JUL-1999;   99WO-US16632.
XX
PR   27-JUL-1998;   98US-0094255.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
PI   Fillmore H,  Broaddus WC,  Gillies GT,  Conrad WS;
XX
DR   WPI; 2000-183137/16.
XX
PT   Preparing antisense oligodeoxynucleotides (ODNs) and long antisense RNA
PT   sequences useful for blocking translation of a specific isoform of
PT   Tenascin-C protein -
XX
PS   Claim 23; Page 102; 177pp; English.
XX
CC   The present invention describes a method for preparing an antisense
CC   oligodeoxynucleotide (ODN) sequence for blocking translation of a
CC   specific protein isoform that can be expressed as a number of different
CC   isoforms. AAA04712 to AAA05243 represent specifically claimed
CC   phosphorothioate antisense ODNs for blocking translation of Tenascin-C
CC   using the method of the invention. The method is useful for preparing
CC   an ODN sequence for blocking translation of a specific isoform of
CC   Tenascin-C protein. The method is also useful for blocking translation
CC   of a specific family of isoforms of a protein. The method can also be
CC   performed by producing a long antisense expression vector encoding a
CC   long antisense RNA sequence for blocking translation of a specific
CC   protein isoform. The ODNs and long antisense constructs are useful in
CC   designing models for studying cellular development and differentiation.
CC   The method permits selective inhibition of the translation of protein
CC   isoforms, which occur as a result of alternative splicing. AAA05244
CC   represent an oligonucleotide from the present invention, which is given
CC   in the sequence listing but not mentioned further within the
CC   specification.
XX
SQ   Sequence 13 BP; 0 A; 5 C; 4 G; 4 T; 0 other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 81;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAG 18
              ||||| ||| |||
Db         13 GGCCAAGCCGAAG 1


RESULT 37
AAA05213/c
ID   AAA05213 standard; DNA; 13 BP.
XX
AC   AAA05213;
XX
DT   18-MAY-2000  (first entry)
XX
DE   Tenascin-C phosphorothioate antisense oligonucleotide SEQ ID NO:502.
XX
KW   Human; Tenascin-C; extracellular matrix protein; phosphorothioate;
KW   antisense oligonucleotide; inhibition; exon deletion; therapy;
KW   cellular development; differentiation; translation; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200006775-A1.
XX
PD   10-FEB-2000.
XX
PF   23-JUL-1999;   99WO-US16632.
XX
PR   27-JUL-1998;   98US-0094255.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
PI   Fillmore H,  Broaddus WC,  Gillies GT,  Conrad WS;
XX
DR   WPI; 2000-183137/16.
XX
PT   Preparing antisense oligodeoxynucleotides (ODNs) and long antisense RNA
PT   sequences useful for blocking translation of a specific isoform of
PT   Tenascin-C protein -
XX
PS   Claim 23; Page 167; 177pp; English.
XX
CC   The present invention describes a method for preparing an antisense
CC   oligodeoxynucleotide (ODN) sequence for blocking translation of a
CC   specific protein isoform that can be expressed as a number of different
CC   isoforms. AAA04712 to AAA05243 represent specifically claimed
CC   phosphorothioate antisense ODNs for blocking translation of Tenascin-C
CC   using the method of the invention. The method is useful for preparing
CC   an ODN sequence for blocking translation of a specific isoform of
CC   Tenascin-C protein. The method is also useful for blocking translation
CC   of a specific family of isoforms of a protein. The method can also be
CC   performed by producing a long antisense expression vector encoding a
CC   long antisense RNA sequence for blocking translation of a specific
CC   protein isoform. The ODNs and long antisense constructs are useful in
CC   designing models for studying cellular development and differentiation.
CC   The method permits selective inhibition of the translation of protein
CC   isoforms, which occur as a result of alternative splicing. AAA05244
CC   represent an oligonucleotide from the present invention, which is given
CC   in the sequence listing but not mentioned further within the
CC   specification.
XX
SQ   Sequence 13 BP; 0 A; 5 C; 4 G; 4 T; 0 other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 81;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAG 18
              ||||| ||| |||
Db         13 GGCCAAGCCGAAG 1


RESULT 38
ABC48592/c
ID   ABC48592 standard; DNA; 13 BP.
XX
AC   ABC48592;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 48609 for detecting SNP TSC0013829.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
```

PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 48609; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 1 A; 1 C; 6 G; 5 T; 0 other;

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 81;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CCAGGCCAAAGTC 20
||| |||||| ||
Db 13 CCACGCCAAAATC 1

RESULT 39
ABC48593
ID ABC48593 standard; DNA; 13 BP.
XX
AC ABC48593;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 48610 for detecting SNP TSC0013829.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 48610; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 5 A; 6 C; 1 G; 1 T; 0 other;

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 81;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CCAGGCCAAAGTC 20
||| |||||| ||
Db 1 CCACGCCAAAATC 13

RESULT 40
AAZ19014
ID AAZ19014 standard; DNA; 11 BP.
XX
AC AAZ19014;
XX
DT 22-OCT-1999 (first entry)
XX
DE Murine MRL SAGE tag 3516811.
XX
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
OS Mus sp.
XX
PN WO9941364-A2.
XX
PD 19-AUG-1999.
XX
PF 12-FEB-1999; 99WO-US02962.
XX
PR 28-SEP-1998; 98US-0102051.
PR 13-FEB-1998; 98US-0074737.
PR 26-AUG-1998; 98US-0097937.
XX
PA (WIST-) WISTAR INST.
XX
PI Heber-Katz E;
XX
DR WPI; 1999-494533/41.
XX
PT New mammalian model for enhanced wound healing - useful for
PT identifying enhanced wound healing genes
XX
PS Claim 13; Page 74; 136pp; English.
XX
CC This invention describes a novel non-MRL healer mouse (M) having at
CC least one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by

```
CC   identifying DNA microsatellite markers which can distinguish healer mice
CC   from non-healer mice and identifying microsatellite markers which
CC   segregate with enhanced wound healing in progeny of the mice, where a
CC   chromosomal locus containing at least one enhanced wound healing gene is
CC   identified. A method of treating a wound in a mammal is also disclosed.
CC   The new methods are useful for treating wounds, especially central and
CC   peripheral nerve wound. The methods of the invention are useful for
CC   restoring function after nerve injury in a mammal. (M) is useful as a
CC   mammalian model of enhanced wound healing, useful for identifying genes
CC   and gene products involved in enhanced wound healing, and to provide
CC   methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC   from C57BL/6 and MRL mice which are used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 11 BP; 1 A; 3 C; 6 G; 1 T; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAGG 12
              ||||||| |||
Db          1 TCCGGGCGAGG 11


RESULT 41
AAX55034/c
ID   AAX55034 standard; DNA; 11 BP.
XX
AC   AAX55034;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              ||||||| |||
Db         11 CCGGGCCGGGC 1


RESULT 42
AAF20603/c
ID   AAF20603 standard; DNA; 11 BP.
XX
AC   AAF20603;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2170.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 264; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
```

```
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              ||||||| |||
Db         11 CCGGGCCGGGC 1


RESULT 43
AAC63229
ID   AAC63229 standard; DNA; 11 BP.
XX
AC   AAC63229;
XX
DT   06-FEB-2001  (first entry)
XX
DE   Oligonucleotide #2 used in a method for primer selection.
XX
KW   PCR primer; nucleic acid amplification; melting temperature; T_m; ss.
XX
OS   Homo sapiens.
XX
PN   WO200060123-A2.
XX
PD   12-OCT-2000.
XX
PF   05-APR-2000; 2000WO-US08962.
XX
PR   06-APR-1999;   99US-0127891.
XX
PA   (GENO-) GENOME TECHNOLOGIES LLC.
XX
PI   Senapathy P;
XX
DR   WPI; 2000-656235/63.
XX
PT   Determining Tm range for several degenerate primers with a
PT   fixed-sequence and a degenerate-sequence portion for use in polymerase
PT   chain reaction amplification by identifying a specific sequence in the
PT   nucleic acid template  -
XX
PS   Disclosure; Fig 2; 34pp; English.
XX
CC   The present invention relates to a method for selecting PCR primers for
CC   nucleic acid amplification. The method comprises determining the melting
CC   temperature (T_m) range for degenerate oligonucleotide primers with a
CC   fixed-sequence portion (FS) and a degenerate-sequence portion (DS) by
CC   searching known portion of a nucleic acid template for a sequence
CC   complementary to a desired FS of a primer. Nucleotide base pairs flanking
CC   or interspersed between the sequence complementary to a DS of one of the
CC   primers are detected and T_m is calculated. The method of the present
CC   invention allows primers which produce more efficient DNA amplification
CC   to be produced. The present sequence is a primer. This sequence was used
CC   to exemplify the occurence of a primer with a FS of 6 base pairs (CGGCCC)
CC   within a template. The remaining 5 base pairs make up the DS.
XX
SQ   Sequence 11 BP; 1 A; 6 C; 4 G; 0 U; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCC 14
              ||| |||||||
Db          1 CGGCCCAGGCC 11


RESULT 44
AAA34481/c
ID   AAA34481 standard; DNA; 11 BP.
XX
AC   AAA34481;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2170.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers  -
XX
PS   Disclosure; Page 537; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
```

```
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              ||||||| |||
Db         11 CCGGGCCGGGC 1


RESULT 45
ABV62380/c
ID   ABV62380 standard; cDNA; 11 BP.
XX
AC   ABV62380;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 166.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 30; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              || ||||||||
Db         11 CCTGGCCAGGC 1


RESULT 46
ABV66640/c
ID   ABV66640 standard; cDNA; 11 BP.
XX
AC   ABV66640;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4426.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 147; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          7 GCCAGGCCAAA 17
              |||| ||||||
Db         11 GCCAAGCCAAA 1


RESULT 47
ABV69801/c
ID   ABV69801 standard; cDNA; 11 BP.
XX
AC   ABV69801;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7587.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Claim 24; Page 240; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 66;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              || ||||||||
Db         11 CCTGGCCAGGC 1


RESULT 48
AAX55033/c
ID   AAX55033 standard; DNA; 12 BP.
XX
AC   AAX55033;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 82;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              ||||||| |||
Db         12 CCGGGCCGGGC 2


RESULT 49
AAF20602/c
ID   AAF20602 standard; DNA; 12 BP.
XX
AC   AAF20602;
XX
```

DT 14-MAR-2001 (first entry)
XX
DE Human C/EBP polynucleotide fragment #2169.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCGGGCCAGGC 13
||||||| |||
Db 12 CCGGGCCGGGC 2

RESULT 50
AAA34480/c
ID AAA34480 standard; DNA; 12 BP.
XX
AC AAA34480;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2169.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 537; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

```
XX
SQ   Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 82;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGC 13
              ||||||| |||
Db         12 CCGGGCCGGGC 2


RESULT 51
AAZ79191/c
ID   AAZ79191 standard; DNA; 10 BP.
XX
AC   AAZ79191;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1619.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 111; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 AGGCCAAAG 18
               |||||||||
Db          10 AGGCCAAAG 2


RESULT 52
AAZ82328/c
ID   AAZ82328 standard; DNA; 10 BP.
XX
AC   AAZ82328;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1562.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
```

PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 100; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGCC 14
|||||||||
Db 9 GGCCAGGCC 1

RESULT 53
AAZ85483
ID AAZ85483 standard; DNA; 10 BP.
XX
AC AAZ85483;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4717.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX

PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 185; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 U; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 AGGCCAAAG 18
|||||||||
Db 2 AGGCCAAAG 10

RESULT 54
AAZ86477/c
ID AAZ86477 standard; DNA; 10 BP.
XX
AC AAZ86477;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5711.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX

```
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 209; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   céll types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGT 19
              |||||||||
Db         10 GGCCAAAGT 2


RESULT 55
AAZ86559/c
ID   AAZ86559 standard; DNA; 10 BP.
XX
AC   AAZ86559;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5793.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 211; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAG 18
              |||||||||
Db         10 AGGCCAAAG 2


RESULT 56
ABL52193/c
ID   ABL52193 standard; DNA; 10 BP.
XX
AC   ABL52193;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Human PER1 preferred oligonucleotide primer SEQ ID NO:118.
XX
KW   Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW   polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW   single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS   Homo sapiens.
XX
```

PN WO200222650-A2.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US28780.
XX
PR 13-SEP-2000; 2000US-232468P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Duda A, Kliem SE, Koshy B;
XX
DR WPI; 2002-393941/42.
XX
PT Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT for therapeutic purposes, for studying the expression and function of
PT the polynucleotide, and for expressing the homolog -
XX
PS Claim 19; Page 15; 162pp; English.
XX
CC The present invention describes an isolated human period (Drosophila)
CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC or its fragment, or a polymorphic variant of a reference sequence
CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC describes methods for genotyping and haplotyping the PER1 gene of an
CC individual. (I) is useful in studying the expression and function of
CC PER1, and in expressing PER1 protein for use in screening for candidate
CC drugs to treat diseases related to PER1 activity. (I) is useful for
CC therapeutic purposes. A recombinant non-human organism transformed or
CC transfected with (I) can be used for studying expression of the PER1
CC isogenes in vivo, for in vivo screening and testing of drugs targeted
CC against PER1 protein, and for testing the efficacy of therapeutic agents
CC and compounds for disorders associated with circadian rhythm regulation.
CC The present sequence represents a preferred oligonucleotide primer
CC for human PER1, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGGGCCAGG 12
||||||||| |
Db 10 CGGGCCAGG 2

RESULT 57
AAS19877/c
ID AAS19877 standard; DNA; 10 BP.
XX
AC AAS19877;
XX
DT 08-MAY-2002 (first entry)
XX
DE Oligonucleotide #57 to detect human RANGAP1 gene polymorphisms.
XX
KW Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KW chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW cancer; irregular cell cycle associated disorder; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200179240-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12455.
XX
PR 17-APR-2000; 2000US-198072P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075068/10.
XX
PT Genotyping human Ran GTPase activating protein 1 gene of individual for
PT determining haplotype of individual, involves determining identity of
PT nucleotide pair at specific polymorphic sites for two copies of the
PT gene -
XX
PS Claim 17; Page 16; 148pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC genotyping the RANGAP1 gene. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the RANGAP1 gene
CC polymorphisms. The polynucleotides and screened compounds are useful for
CC treatment of diseases associated with RANGAP1 activity, such as
CC cancer and other disorders associated with an irregular cell cycle.
CC AAS19821-AAS19898 represent primer-extension oligonucleotides for
CC detecting human RANGAP1 gene polymorphisms.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGGGCCAGG 12
||||||||| |
Db 10 CGGGCCAGG 2

RESULT 58
AAD26166
ID AAD26166 standard; DNA; 10 BP.
XX
AC AAD26166;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human endothelin 2 (EDN2) gene polymorphism detecting primer #5.
XX
KW Human; endothelin 2; EDN2; polymorphic site; PS; therapy; hypertension;
KW drug screening; cardiovascular disorder; renal insufficiency; ASO;
KW allele specific oligonucleotide; cerebroprotective; polymorphism;
KW hypotensive; cerebrovascular condition; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190118-A2.
XX
PD 29-NOV-2001.
XX
PF 21-MAY-2001; 2001WO-US16433.
XX
PR 19-MAY-2000; 2000US-205761P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Koshy B, Tanguay DA;
XX
DR WPI; 2002-083075/11.
XX
PT New human endothelin 2 (EDN2) polymorphic variants and encoding genes,
PT useful in expressing EDN2 protein for screening candidate drugs to
PT treat diseases related to EDN2 activity -
XX
PS Claim 18; Page 15; 91pp; English.
XX

```
CC   The invention relates to genetic variants of human endothelin 2 (EDN2)
CC   gene. EDN2 gene contains 17 polymorphic sites PS1-PS17. The polymorphic
CC   variants are useful in studying the expression and function of EDN2,
CC   in expressing EDN2 protein for use in screening for candidate drugs to
CC   treat diseases related to EDN2 activity, in studying the effect of the
CC   variation on the biological activity of EDN2, and the binding affinity
CC   of candidate drugs targetting EDN2 for the treatment of hypertension,
CC   cardiovascular disorders, renal insufficiency and cerebrovascular
CC   conditions. The haplotyping methods are useful in validating EDN2 as
CC   a candidate target for treating a specific condition or disease
CC   predicted to be associated with EDN2 activity, or in the design of
CC   clinical trials of candidate drugs for treating a specific condition
CC   or disease associated with EDN2 activity. Allele specific
CC   oligonucleotides (ASO) are used as probes and primers, and for
CC   detecting polymorphism in EDN2 gene. The present sequence is a
CC   primer used to detect polymorphism in human EDN2 gene.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGG 12
              |||||||||
Db          2 CGGGCCAGG 10


RESULT 59
ABQ81865/c
ID   ABQ81865 standard; DNA; 11 BP.
XX
AC   ABQ81865;
XX
DT   19-NOV-2002  (first entry)
XX
DE   Kaposi's Sarcoma SAGE library Tag No.15 SEQ ID NO:15.
XX
KW   Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss.
XX
OS   Homo sapiens.
XX
PN   EP1225233-A2.
XX
PD   24-JUL-2002.
XX
PF   23-JAN-2002; 2002EP-0075264.
XX
PR   23-JAN-2001; 2001EP-0200228.
PR   28-SEP-2001; 2001EP-0203703.
PR   28-SEP-2001; 2001US-325722P.
XX
PA   (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
PI   Van Der Kuyl AC,  Cornelissen M;
XX
DR   WPI; 2002-668396/72.
XX
PT   Determining presence of a tumor cell or angiogenesis, and the
PT   effectiveness of treatment, by detecting the presence of marker genes
PT   is useful to detect and monitor treatment of Kaposi's Sarcoma  -
XX
PS   Claim 12; Page 8; 38pp; English.
XX
CC   The present invention describes a method for determining if an individual
CC   has a tumour cell or site of angiogenesis, or if a treatment is effective
CC   in changing angiogenesis or changing a status of a set of target cells,
CC   comprising determining if a sample of the subject has an expression
CC   product of at least one marker gene. Also described is a compound capable
CC   of altering the expression or activity of Keratin 14, TIE 1, Salioadhesin
CC   or Siglec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed
CC   Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from
CC   the present invention can be used in a diagnostic method, particularly as
CC   an indicator of angiogenesis or to determine presence of a tumour cell.
CC   The method of the invention is suitable to determine within a few days if
CC   a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to
CC   ABQ82006 represent nucleotide sequence used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||||||||
Db         11 GGCCAGGCC 3


RESULT 60
ABV62890/c
ID   ABV62890 standard; cDNA; 11 BP.
XX
AC   ABV62890;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 676.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 44; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAA 17
```

```
              |||||||||
Db          10 CAGGCCAAA 2


RESULT 61
ABV64419/c
ID   ABV64419 standard; cDNA; 11 BP.
XX
AC   ABV64419;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2205.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 86; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAA 16
              |||||||||
Db         11 CCAGGCCAA 3


RESULT 62
ABV64637/c
ID   ABV64637 standard; cDNA; 11 BP.
XX
AC   ABV64637;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2423.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 92; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||||||||
Db         11 GGCCAGGCC 3


RESULT 63
ABV68400/c
ID   ABV68400 standard; cDNA; 11 BP.
XX
AC   ABV68400;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6186.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
```

PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 197; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCAA 16
|||||||||
Db 11 CCAGGCCAA 3

RESULT 64
ABV68594/c
ID ABV68594 standard; cDNA; 11 BP.
XX
AC ABV68594;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6380.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 202; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 0 A; 2 C; 5 G; 4 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCAA 16
|||||||||
Db 10 CCAGGCCAA 2

RESULT 65
ABV70311/c
ID ABV70311 standard; cDNA; 11 BP.
XX
AC ABV70311;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8097.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Claim 24; Page 258; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.

```
XX
SQ   Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAA 17
              |||||||||
Db         10 CAGGCCAAA 2


RESULT 66
ABV71840/c
ID   ABV71840 standard; cDNA; 11 BP.
XX
AC   ABV71840;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9626.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Claim 24; Page 311; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAA 16
              |||||||||
Db         11 CCAGGCCAA 3


RESULT 67
AAS19798/c
ID   AAS19798 standard; DNA; 15 BP.
XX
AC   AAS19798;
XX
DT   08-MAY-2002  (first entry)
XX
DE   ASO primer #56 to detect human RANGAP1 gene polymorphisms.
XX
KW   Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KW   chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW   cancer; irregular cell cycle associated disorder; ASO; primer; ss;
KW   allele-specific oligonucleotide.
XX
OS   Homo sapiens.
XX
PN   WO200179240-A2.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-US12455.
XX
PR   17-APR-2000; 2000US-198072P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-075068/10.
XX
PT   Genotyping human Ran GTPase activating protein 1 gene of individual for
PT   determining haplotype of individual, involves determining identity of
PT   nucleotide pair at specific polymorphic sites for two copies of the
PT   gene  -
XX
PS   Claim 15; Page 15; 148pp; English.
XX
CC   The present invention relates to novel single nucleotide polymorphisms
CC   (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC   located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC   genotyping the RANGAP1 gene. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC   primer-extension oligonucleotides for detecting the RANGAP1 gene
CC   polymorphisms. The polynucleotides and screened compounds are useful for
CC   treatment of diseases associated with RANGAP1 activity, such as
CC   cancer and other disorders associated with an irregular cell cycle.
CC   AAS19743-AAS19820 represent ASO primers for detecting human RANGAP1
CC   gene polymorphisms.
XX
SQ   Sequence 15 BP; 3 A; 6 C; 5 G; 0 U; 1 other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 15;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGG 12
              |||| |||| ||
Db         12 GTCCTGGCCCGG 1


RESULT 68
AAV60744/c
ID   AAV60744 standard; DNA; 18 BP.
XX
AC   AAV60744;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Primer #2 for human CDK4 codons 1-163.
XX
KW   PCR primer; amplification; yeast; UAS; upstream activating sequence;
KW   transcription terminator; cell cycle; Upstream Activation Sequence; UAS;
KW   promoter; phosphorylation; cyclin; cyclin-dependent kinase; CDK; vector;
```

```
KW   cyclin kinase inhibitor; CKI; growth; wound healing; cancer therapy; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9816660-A1.
XX
PD   23-APR-1998.
XX
PF   16-OCT-1997;   97WO-US18608.
XX
PR   27-NOV-1996;   96US-0031968.
PR   16-OCT-1996;   96US-0029127.
XX
PA   (BITT-) BITTECH INC.
XX
PI   Bitter GA;
XX
DR   WPI; 1998-251302/22.
XX
PT   Screening for agents that effect cell cycle regulatory proteins -
PT   using a cell line that expresses a reporter gene in response to
PT   regulation through phosphorylation by a cyclin/CDK system
XX
PS   Example 4; Page 75; 93pp; English.
XX
CC   Primers AAV60743-V60745 were used to PCR amplify codons 1-163 of the
CC   human cyclin-dependent kinase 4 (hCDK4). The amplified product was used
CC   to generate a fusion protein comprising part of the hCDK4 sequence
CC   linked to codons 154-302 of the yeast PHO85 gene. The fusion protein is
CC   used to screen for compounds that affect mammalian cell cycle regulatory
CC   proteins. The method comprises administering a compound to a cell line,
CC   which contains a reporter gene linked to an Upstream Activation Sequence
CC   (UAS) and a promoter, where the UAS binds a transcription control factor
CC   (TCF) which is regulated through cyclin/cyclin-dependent kinase (CDK)
CC   phosphorylation. Also included in the construct is an effector gene
CC   providing a gene product to permit normal cyclin/CDK regulation of the
CC   TCF. Expression of the reporter gene is then analysed in the cell line,
CC   thereby determining whether the compound affects the normal regulation.
CC   The method can be used to identify inhibitors and activators of
CC   mammalian cell cycle regulatory proteins, especially inhibitors and
CC   activators of cyclins, CDKs, cyclin/CDK complexes, cyclin kinase
CC   inhibitors (CKIs), and cyclin/CDK/CKI complexes. The identified agents
CC   can be used for stimulating growth of cells (as in wound healing), or
CC   regulating excessive cell growth and division (as in cancer therapy).
XX
SQ   Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAA 17
              |||| ||||| |
Db         12 GGCCTGGCCAGA 1


RESULT 69
AAQ96791
ID   AAQ96791 standard; DNA; 10 BP.
XX
AC   AAQ96791;
XX
DT   26-MAR-1996  (first entry)
XX
DE   HIV-1 NL4-3 nef gene nucleotide deletion 386.
XX
KW   HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO9521912-A1.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-AU00063.
XX
PR   23-DEC-1994;   94AU-0000284.
PR   14-FEB-1994;   94AU-0003864.
PR   21-FEB-1994;   94AU-0004002.
XX
PA   (AURE-) AUSTRALIAN RED CROSS SOC NSW DIV.
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI   Cooper D,  Crowe S,  Deacon NJ,  Learmont JC,  McPhee DA;
XX
DR   WPI; 1995-293115/38.
XX
PT   New non-pathogenic HIV-1 strain carrying a deletion in its nef gene
PT   or LTR region  - can be used in a vaccine to inhibit/reduce
PT   productive infection in an individual by a pathogenic strain
XX
PS   Claim 13; Page 193; 301pp; English.
XX
CC   Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1
CC   or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or
CC   1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the
CC   sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene
CC   (AAQ96141).  The resulting avirulent HIV strains are still capable of
CC   inducing an immune response in humans, and enable the generation of
CC   therapeutic, diagnostic and targeting agents against HIV-1 infection.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 5 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              | ||||||||
Db          1 CAGGGCCAGG 10


RESULT 70
AAT29327/c
ID   AAT29327 standard; DNA; 10 BP.
XX
AC   AAT29327;
XX
DT   25-MAR-2003  (updated)
DT   28-JUN-1996  (first entry)
XX
DE   5'-primer for mammalian G-protein coupled receptor coding sequences.
XX
KW   5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
```

```
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Claim 46; Page 55; 72pp; English.
XX
CC   The 5'-primers AAT29262-382, and the complementary 3'-primers derived
CC   from them, which target mammalian G-protein coupled receptor coding
CC   sequences, together comprise a PCR primer kit. The kit is used in a
CC   new method for the characterisation of nucleic acid sequences obtd.
CC   from mammalian biological samples, which comprises PCR amplification
CC   and indexing of the prods. w.r.t the primer pair that hybridised to
CC   its delineating subsequences. The method may be used in the
CC   identification, cloning and analysis of genes, e.g. in genome
CC   mapping, and disease diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||||||
Db         10 CAGGCCAGGC 1


RESULT 71
AAV50125/c
ID   AAV50125 standard; DNA; 10 BP.
XX
AC   AAV50125;
XX
DT   21-OCT-1998  (first entry)
XX
DE   Yeast tag for NORF gene locus NORF15.
XX
KW   Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle;
KW   regulation; eukaryotic cell; antifungal; SAGE tag; gene expression;
KW   serial analysis of gene expression; probe; ss.
XX
OS   Saccharomyces cerevisiae.
OS   Synthetic.
XX
PN   WO9832847-A2.
XX
PD   30-JUL-1998.
XX
PF   22-JAN-1998;   98WO-US01216.
XX
PR   23-JAN-1997;   97US-0035917.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Kinzler KW,  Velculescu VE,  Vogelstein B;
XX
DR   WPI; 1998-427943/36.
XX
PT   Yeast transcriptome - useful for modulating eukaryotic cell, for
PT   screening antifungal agents, and for identifying genes in cell cycle
PT   progression
XX
PS   Claim 1; Page 23; 44pp; English.
XX
CC   Yeast transcriptome is encoded by a DNA molecule comprising a yeast
CC   gene involved in cell cycle progression selected from the group of
CC   nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC   tags for highly expressed genes and NORF genes are given in AAV50051 to
CC   AAV50345. The present invention describes: (1) a method of using yeast
CC   genes to modulate the cell cycle which comprises administering to a cell
CC   an isolated DNA molecule comprising a yeast gene which is involved in
CC   cell cycle progression selected from differentially expressed genes
CC   (SAGE tags given in AAV50051 to AAV50345); (2) a method for screening
CC   candidate antifungal drugs which comprises contacting a test substance
CC   with a yeast cell and monitoring expression of a yeast gene which is
CC   involved in cell cycle progression; (3) a method of identifying human
CC   genes which are involved in cell cycle progression which comprises
CC   hybridizing a probe comprising at least 10 contiguous nucleotides of a
CC   yeast gene which is differentially expressed between at least 2 phases
CC   selected from the log phase, the S phase and the G2/M phase; and (4) a
CC   probe for ascertaining the phase in the cell cycle, where the probe
CC   comprises at least 14 contiguous nucleotides of a NORF gene (SAGE tags
CC   given in AAV50051 to AAV50345), or as an array of probes on a solid
CC   support.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              ||||||| ||
Db         10 GGCCAGGGCA 1


RESULT 72
AAX54917
ID   AAX54917 standard; DNA; 10 BP.
XX
AC   AAX54917;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 68; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
```

```
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 6 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| |||
Db          1 CGGGCCGGGC 10


RESULT 73
AAF20486
ID   AAF20486 standard; DNA; 10 BP.
XX
AC   AAF20486;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2053.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 262; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 6 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| |||
Db          1 CGGGCCGGGC 10


RESULT 74
AAC73935/c
ID   AAC73935 standard; cDNA; 10 BP.
XX
AC   AAC73935;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human dendritic cell cDNA base sequence oligonucleotide #22.
XX
KW   Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW   autoimmune disease; tumour; ss.
XX
OS   Homo sapiens.
XX
PN   WO200060074-A1.
XX
PD   12-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-JP02019.
XX
PR   01-APR-1999;   99JP-0095481.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Hashimoto S,  Matsushima K,  Suzuki T;
XX
DR   WPI; 2000-619172/59.
XX
PT   Groups of genes expressed in human dendritic cells at a greater or
PT   lesser extent than in monocytes for investigation and diagnosis of
PT   autoimmune disease and tumors  -
XX
PS   Claim 1; Page 9; 95pp; Japanese.
XX
CC   The present invention describes a group of genes consisting of 100 genes
```

```
CC   which are highly expressed in human dendritic cells; a group of genes
CC   which are expressed at a higher frequency in human dendritic cells than
CC   in human monocytes; and a group of genes which are expressed at lower
CC   frequency in human dendritic cells than in human monocytes. Each group
CC   of genes are characterised in that cDNAs of these genes respectively
CC   have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
CC   SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
CC   (AAC74114 to AAC74213), each is continuous with the base sequence
CC   5'-CATG-3' located most closely to the poly-A region. The sequences can
CC   be used for the investigation of the role and mechanism of the
CC   involvement of dendritic cells in the immune system and for the study and
CC   diagnosis of diseases in which dendritic cells play a significant role,
CC   e.g. cancers and autoimmune diseases.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 75
AAC74189/c
ID   AAC74189 standard; cDNA; 10 BP.
XX
AC   AAC74189;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human monocyte and dendritic cell expressed gene oligonucleotide #276.
XX
KW   Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW   autoimmune disease; tumour; ss.
XX
OS   Homo sapiens.
XX
PN   WO200060074-A1.
XX
PD   12-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-JP02019.
XX
PR   01-APR-1999;   99JP-0095481.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Hashimoto S,  Matsushima K,  Suzuki T;
XX
DR   WPI; 2000-619172/59.
XX
PT   Groups of genes expressed in human dendritic cells at a greater or
PT   lesser extent than in monocytes for investigation and diagnosis of
PT   autoimmune disease and tumors  -
XX
PS   Claim 19; Page 16; 95pp; Japanese.
XX
CC   The present invention describes a group of genes consisting of 100 genes
CC   which are highly expressed in human dendritic cells; a group of genes
CC   which are expressed at a higher frequency in human dendritic cells than
CC   in human monocytes; and a group of genes which are expressed at lower
CC   frequency in human dendritic cells than in human monocytes. Each group
CC   of genes are characterised in that cDNAs of these genes respectively
CC   have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
CC   SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
CC   (AAC74114 to AAC74213), each is continuous with the base sequence
CC   5'-CATG-3' located most closely to the poly-A region. The sequences can
CC   be used for the investigation of the role and mechanism of the
CC   involvement of dendritic cells in the immune system and for the study and
CC   diagnosis of diseases in which dendritic cells play a significant role,
CC   e.g. cancers and autoimmune diseases.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 76
AAA34364
ID   AAA34364 standard; DNA; 10 BP.
XX
AC   AAA34364;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2053.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers  -
XX
PS   Disclosure; Page 523; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
```

```
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 6 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| |||
Db          1 CGGGCCGGGC 10


RESULT 77
AAZ77977/c
ID   AAZ77977 standard; DNA; 10 BP.
XX
AC   AAZ77977;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:405.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 76; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||||| |
Db         10 GCCAGGCCCA 1


RESULT 78
AAZ78898
ID   AAZ78898 standard; DNA; 10 BP.
XX
AC   AAZ78898;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1326.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
```

PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13800.
XX
PR 19-JUN-1998; 98US-0089833.
PR 19-JUN-1998; 98US-0089844.
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089878.
PR 19-JUN-1998; 98US-0089991.
PR 19-JUN-1998; 98US-0089992.
PR 19-JUN-1998; 98US-0089993.
PR 19-JUN-1998; 98US-0089994.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0089999.
PR 19-JUN-1998; 98US-0090000.
PR 19-JUN-1998; 98US-0090035.
PR 19-JUN-1998; 98US-0090036.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PR 19-JUN-1998; 98US-0090042.
PR 19-JUN-1998; 98US-0090043.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090045.
PR 19-JUN-1998; 98US-0090047.
PR 19-JUN-1998; 98US-0090048.
PR 19-JUN-1998; 98US-0090072.
PR 19-JUN-1998; 98US-0090076.
PR 19-JUN-1998; 98US-0090077.
PR 19-JUN-1998; 98US-0090078.
PR 19-JUN-1998; 98US-0090079.
PR 19-JUN-1998; 98US-0090080.
PR 08-DEC-1998; 98US-0111715.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer -
XX
PS Claim 1; Page 103; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or
CC ESTs (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can
CC lyse the tumour cells, immunostimulatory cofactors also being required
CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell
CC differentially expressed genes, or of their encoded proteins, can be used
CC to identify cells as belonging to the monocyte lineage. Cells containing
CC these genes can be used in active immunotherapy (or to stimulate
CC production of a population of antigen-specific effector cells) and
CC vectors containing them are used in gene therapy. Co-administration of
CC tumour antigens and APC-associated costimulatory factors ensures adequate
CC antigen presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells.
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AGGCCAAAGT 19
|| |||||||
Db 1 AGACCAAAGT 10

RESULT 79
AAZ81571
ID AAZ81571 standard; DNA; 10 BP.
XX
AC AAZ81571;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #805.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 79; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while

CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AGGCCAAAGT 19
|| |||||||
Db 1 AGACCAAAGT 10

RESULT 80
AAZ82444/c
ID AAZ82444 standard; DNA; 10 BP.
XX
AC AAZ82444;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1678.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 103; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCA 15
|| |||||||
Db 10 GGGCAGGCCA 1

RESULT 81
AAZ82611/c
ID AAZ82611 standard; DNA; 10 BP.
XX
AC AAZ82611;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1845.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 108; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,

```
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              ||||| ||||
Db         10 CCAGGACAAA 1


RESULT 82
AAZ82634
ID   AAZ82634 standard; DNA; 10 BP.
XX
AC   AAZ82634;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1868.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 109; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              |||||||| |
Db          1 GGCCAAAGGC 10


RESULT 83
AAZ82905/c
ID   AAZ82905 standard; DNA; 10 BP.
XX
AC   AAZ82905;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2139.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 117; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
```

CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCCAGGCC 14
||||||| ||
Db 10 GGGCCAGTCC 1

RESULT 84
AAZ83555/c
ID AAZ83555 standard; DNA; 10 BP.
XX
AC AAZ83555;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2789.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 133; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCGGGCCAGG 12
| ||||||||
Db 10 CAGGGCCAGG 1

RESULT 85
AAZ84116
ID AAZ84116 standard; DNA; 10 BP.
XX
AC AAZ84116;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3350.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 148; 219pp; English.

```
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 6 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||| ||||||
Db          1 GGGGCAGGCC 10


RESULT 86
AAZ84369/c
ID   AAZ84369 standard; DNA; 10 BP.
XX
AC   AAZ84369;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3603.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 155; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              |||||| |||
Db         10 GGGCCAAGCC 1


RESULT 87
AAZ84683
ID   AAZ84683 standard; DNA; 10 BP.
XX
AC   AAZ84683;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3917.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
```

```
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 163; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour.
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 4 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              || |||||||
Db          1 GGCCCAGGCC 10


RESULT 88
AAZ84966/c
ID   AAZ84966 standard; DNA; 10 BP.
XX
AC   AAZ84966;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4200.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 171; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||||| |
Db         10 GCCAGGCCCA 1


RESULT 89
AAZ85815/c
ID   AAZ85815 standard; DNA; 10 BP.
XX
AC   AAZ85815;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5049.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
```

```
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 193; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCCGGCCAA 1


RESULT 90
AAZ85951
ID   AAZ85951 standard; DNA; 10 BP.
XX
AC   AAZ85951;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5185.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 196; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 4 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||||||| ||
Db          1 GGGCCAGCCC 10


RESULT 91
AAZ86053/c
ID   AAZ86053 standard; DNA; 10 BP.
XX
AC   AAZ86053;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5287.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
```

```
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 199; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||||||
Db         10 CAGGCCAGGC 1


RESULT 92
AAI67394/c
ID   AAI67394 standard; DNA; 10 BP.
XX
AC   AAI67394;
XX
DT   11-FEB-2002  (first entry)
XX
DE   Human FKBP8 gene polymorphism detecting primer.
XX
KW   FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
KW   immunosuppression; human; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200172965-A2.
XX
PD   04-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-US09718.
XX
PR   24-MAR-2000; 2000US-192125P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Bentivegna SC,  Choi JY,  Kliem SE,  Koshy B;
PI   Stephens JC;
XX
DR   WPI; 2001-626261/72.
XX
PT   New haplotypes of the FK506-binding protein 8 gene, useful for
PT   genotyping that gene in individual and to design new therapy for
PT   associated disease such as immunosuppression and cancer  -
XX
PS   Claim 16; Page 15; 98pp; English.
XX
CC   The invention relates to haplotyping the FK506-binding protein 8 (38kD)
CC   (FKBP8) gene in an individual. The method involves determining the
CC   identity of the nucleotide pair at one or more polymorphic sites selected
CC   from P1 to P26 ( described in the specification). The invention is useful
CC   to improve the efficiency and reliability of several steps in the
CC   discovery and development of drugs for treating diseases associated with
CC   FKBP8 activity, for example immunosuppression and cancer. Sequences
CC   AAI67352-403 represent oligonucleotide primers for detecting FKBP8 gene
CC   polymorphisms by primer extension techniques.
XX
SQ   Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              |||||||| |
Db         10 CCAGGCCACA 1


RESULT 93
ABA06204/c
ID   ABA06204 standard; cDNA; 10 BP.
XX
AC   ABA06204;
XX
DT   10-JAN-2002  (first entry)
XX
DE   Human normal hepatocyte expression gene cDNA, SEQ ID NO: 181.
XX
KW   Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001211883-A.
XX
PD   07-AUG-2001.
XX
PF   31-JAN-2000; 2000JP-0023170.
XX
PR   31-JAN-2000; 2000JP-0023170.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-629566/73.
XX
PT   Human normal hepatocyte expression gene group  -
XX
PS   Claim 1; Page 9; 26pp; Japanese.
XX
CC   The invention relates to a human normal hepatocyte expression gene
CC   group comprising 200 genes in the human normal hepatocyte. The
CC   cDNA of each gene comprises one of 200 fully defined nucleotide
CC   sequences as given in the specification. The gene group and the cDNAs
CC   corresponding to each of the genes in the group are useful in the
CC   diagnosis and treatment of human hepatopathy. The present sequence
CC   is a cDNA corresponding to a gene expressed by normal human
CC   hepatocytes.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
```

```
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 94
AAH76342/c
ID   AAH76342 standard; DNA; 10 BP.
XX
AC   AAH76342;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Z. mays Ms45 promoter deletion mutant fragment LS02.
XX
KW   Ms45; male tissue; regulatory region; transcription; male fertility;
KW   hybrid seed; promoter; ss.
XX
OS   Zea mays.
XX
PN   WO200160997-A2.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04527.
XX
PR   15-FEB-2000; 2000US-0504487.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Albertsen MC,  Fox TW,  Garnaat CW,  Huffman G,  Kendall TL;
XX
DR   WPI; 2001-514772/56.
XX
PT   A male tissue-preferred regulatory region comprising nucleotide
PT   sequences essential for initiating transcription of the MS45 gene
PT   useful for mediating fertility in a male plant -
XX
PS   Example 5; Fig 8; 50pp; English.
XX
CC   The invention provides a male tissue-preferred regulatory region (I)
CC   comprising nucleotide sequences essential for initiating transcription
CC   of the MS45 gene. A method of mediating male fertility in a plant is
CC   provided that involves introducing an expression vector comprising a
CC   promoter operably linked to (I) into a plant where the exogenous gene
CC   impacts male fertility of the plant and (I) controls expression of the
CC   exogenous gene. A method of producing hybrid seeds is also provided.
CC   Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC   promoter region, used for determining the essential region of MS45
CC   promoter.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| |||
Db         10 CGGGCCCGGC 1


RESULT 95
AAH76345
ID   AAH76345 standard; DNA; 10 BP.
XX
AC   AAH76345;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Z. mays Ms45 promoter deletion mutant fragment LS05.
XX
KW   Ms45; male tissue; regulatory region; transcription; male fertility;
KW   hybrid seed; promoter; ss.
XX
OS   Zea mays.
XX
PN   WO200160997-A2.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04527.
XX
PR   15-FEB-2000; 2000US-0504487.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Albertsen MC,  Fox TW,  Garnaat CW,  Huffman G,  Kendall TL;
XX
DR   WPI; 2001-514772/56.
XX
PT   A male tissue-preferred regulatory region comprising nucleotide
PT   sequences essential for initiating transcription of the MS45 gene
PT   useful for mediating fertility in a male plant -
XX
PS   Example 5; Fig 8; 50pp; English.
XX
CC   The invention provides a male tissue-preferred regulatory region (I)
CC   comprising nucleotide sequences essential for initiating transcription
CC   of the MS45 gene. A method of mediating male fertility in a plant is
CC   provided that involves introducing an expression vector comprising a
CC   promoter operably linked to (I) into a plant where the exogenous gene
CC   impacts male fertility of the plant and (I) controls expression of the
CC   exogenous gene. A method of producing hybrid seeds is also provided.
CC   Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC   promoter region, used for determining the essential region of MS45
CC   promoter.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| |||
Db          1 CGGGCCCGGC 10


RESULT 96
AAH76348/c
ID   AAH76348 standard; DNA; 10 BP.
XX
AC   AAH76348;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Z. mays Ms45 promoter deletion mutant fragment LS08.
XX
KW   Ms45; male tissue; regulatory region; transcription; male fertility;
KW   hybrid seed; promoter; ss.
XX
OS   Zea mays.
XX
PN   WO200160997-A2.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04527.
XX
PR   15-FEB-2000; 2000US-0504487.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
```

```
PI   Albertsen MC,  Fox TW,  Garnaat CW,  Huffman G,  Kendall TL;
XX
DR   WPI; 2001-514772/56.
XX
PT   A male tissue-preferred regulatory region comprising nucleotide
PT   sequences essential for initiating transcription of the MS45 gene
PT   useful for mediating fertility in a male plant -
XX
PS   Example 5; Fig 8; 50pp; English.
XX
CC   The invention provides a male tissue-preferred regulatory region (I)
CC   comprising nucleotide sequences essential for initiating transcription
CC   of the MS45 gene. A method of mediating male fertility in a plant is
CC   provided that involves introducing an expression vector comprising a
CC   promoter operably linked to (I) into a plant where the exogenous gene
CC   impacts male fertility of the plant and (I) controls expression of the
CC   exogenous gene. A method of producing hybrid seeds is also provided.
CC   Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC   promoter region, used for determining the essential region of MS45
CC   promoter.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||||| ||||
Db         10 GGGCCCGGCC 1


RESULT 97
AAH63580/c
ID   AAH63580 standard; cDNA; 10 BP.
XX
AC   AAH63580;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 420.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 48; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 98
AAH63581/c
ID   AAH63581 standard; cDNA; 10 BP.
XX
AC   AAH63581;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 421.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 48; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 99
AAH63582
ID   AAH63582 standard; cDNA; 10 BP.
XX
```

AC AAH63582;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 422.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
PS Claim 13; Page 48; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GGCCAAAGTC 20
|||||||| |
Db 1 GGCCAAAGGC 10

RESULT 100
AAH63804
ID AAH63804 standard; cDNA; 10 BP.
XX
AC AAH63804;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 644.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
PS Claim 13; Page 53; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AGGCCAAAGT 19
|| |||||||
Db 1 AGACCAAAGT 10

RESULT 101
AAH64388/c
ID AAH64388 standard; cDNA; 10 BP.
XX
AC AAH64388;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1228.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
PS Claim 13; Page 67; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce

```
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 102
AAH64389/c
ID   AAH64389 standard; cDNA; 10 BP.
XX
AC   AAH64389;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1229.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 103
AAH64390/c
ID   AAH64390 standard; cDNA; 10 BP.
XX
AC   AAH64390;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1230.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 104
AAH64391/c
ID   AAH64391 standard; cDNA; 10 BP.
XX
AC   AAH64391;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1231.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
```

```
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 105
AAH64392/c
ID   AAH64392 standard; cDNA; 10 BP.
XX
AC   AAH64392;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1232.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 106
AAH64393/c
ID   AAH64393 standard; cDNA; 10 BP.
XX
AC   AAH64393;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1233.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 107
AAH64394/c
```

```
ID   AAH64394 standard; cDNA; 10 BP.
XX
AC   AAH64394;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1234.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 108
AAH32882/c
ID   AAH32882 standard; cDNA; 10 BP.
XX
AC   AAH32882;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:255.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001069993-A.
XX
PD   21-MAR-2001.
XX
PF   28-APR-2000; 2000JP-0131079.
XX
PR   08-JUL-1999;   99JP-0195103.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-304369/32.
XX
PT   LPS activated human monocyte expression gene group  -
XX
PS   Claim 19; Page 42; 52pp; Japanese.
XX
CC   The present invention describes an lipopolysaccharide (LPS) activated
CC   human monocyte expression gene group consisting of the high-ranking 50
CC   genes of the highest expression among the genes expressed by human
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC   development of new means for the diagnosis and the treatment of various
CC   human diseases in which human monocyte plays an important role.
CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC   monocyte expression gene cDNA tags from the present invention. AAH32944
CC   represents an LPS activated human monocyte expression gene cDNA sequence
CC   encoding AAB98009, which are given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 109
AAF74058/c
ID   AAF74058 standard; DNA; 10 BP.
XX
AC   AAF74058;
XX
DT   30-APR-2001  (first entry)
XX
DE   Human SLC6A4 allele-specific oligonucleotide primer #178.
XX
KW   Solute carrier family 6 neurotransmiter transporter; seotonin 4;
KW   SLC6A4; genotyping; allele specific oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109161-A1.
XX
PD   08-FEB-2001.
XX
PF   31-JUL-2000; 2000WO-US20638.
XX
PR   29-JUL-1999;   99US-0146290.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Denton RR,  Duda A,  Nandabalan K,  Sanchis A,  Stephens JC;
XX
DR   WPI; 2001-123317/13.
XX
PT   New isolated polynucleotide comprising a polymorphic variant  for the
PT   solute carrier family 6 neurotransmitter transporter, serotonin member
PT   4 gene for  identifying drugs for treating disorders related to
PT   expression of the protein  -
XX
PS   Disclosure; Page 23; 152pp; English.
XX
CC   The present invention relates to a polymorphic variant of a reference
```

```
CC   sequence for the solute carrier family 6 neurotransmitter
CC   transporter, serotonin member 4 (SLC6A4) gene or a fragment of it
CC   or a sequence complementary to the first sequence.
CC   The invention is used in producing a recombinant organism
CC   that can be used to express SLC6A4 for protein structure analysis and
CC   binding studies.  A composition comprising a genotyping oligonucleotide
CC   is used to detect a polymorphism in the SLC6A4 gene.
XX
SQ   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCA 10
              ||| ||||||
Db         10 GTCTGGGCCA 1


RESULT 110
AAF33342/c
ID   AAF33342 standard; DNA; 10 BP.
XX
AC   AAF33342;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:81.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis
PT   of gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle -
XX
PS   Claim 1; Page 23; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
CC   progression comprising contacting human DNA with a probe which comprises
CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC   member of a class of drugs having a characteristic effect on gene
CC   expression in a yeast cell comprising contacting a yeast cell with a
CC   candidate drug and monitoring expression in the yeast cell of at least 1
CC   NORF gene whose expression is affected by the class of drugs. The NORF
CC   genes may be used to study, monitor and affect phases of the cell cycle,
CC   the differentially expressed genes may be used as markers of phases of
CC   the cell cycle. The methods may be used to identify candidate drugs which
CC   affect the cell cycle and for identification of antifungal drugs.
CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC   primers used in the SAGE method, in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              ||||||| ||
Db         10 GGCCAGGGCA 1


RESULT 111
AAF33708/c
ID   AAF33708 standard; DNA; 10 BP.
XX
AC   AAF33708;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:447.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis
PT   of gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle -
XX
PS   Claim 1; Page 391; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
```

CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCA 15
||||||| ||
Db 10 GGCCAGGGCA 1

RESULT 112
AAF34406/c
ID AAF34406 standard; DNA; 10 BP.
XX
AC AAF34406;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1145.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 40; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCA 15
||||||| ||
Db 10 GGCCAGGGCA 1

RESULT 113
AAF35939/c
ID AAF35939 standard; DNA; 10 BP.
XX
AC AAF35939;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2678.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 95; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell

```
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
CC   progression comprising contacting human DNA with a probe which comprises
CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC   member of a class of drugs having a characteristic effect on gene
CC   expression in a yeast cell comprising contacting a yeast cell with a
CC   candidate drug and monitoring expression in the yeast cell of at least 1
CC   NORF gene whose expression is affected by the class of drugs. The NORF
CC   genes may be used to study, monitor and affect phases of the cell cycle,
CC   the differentially expressed genes may be used as markers of phases of
CC   the cell cycle. The methods may be used to identify candidate drugs which
CC   affect the cell cycle and for identification of antifungal drugs.
CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC   primers used in the SAGE method, in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              ||||||| ||
Db         10 GGCCAAACTC 1


RESULT 114
AAF41896/c
ID   AAF41896 standard; DNA; 10 BP.
XX
AC   AAF41896;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8635.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis
PT   of gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle -
XX
PS   Example; Page 308; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
CC   progression comprising contacting human DNA with a probe which comprises
CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC   member of a class of drugs having a characteristic effect on gene
CC   expression in a yeast cell comprising contacting a yeast cell with a
CC   candidate drug and monitoring expression in the yeast cell of at least 1
CC   NORF gene whose expression is affected by the class of drugs. The NORF
CC   genes may be used to study, monitor and affect phases of the cell cycle,
CC   the differentially expressed genes may be used as markers of phases of
CC   the cell cycle. The methods may be used to identify candidate drugs which
CC   affect the cell cycle and for identification of antifungal drugs.
CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC   primers used in the SAGE method, in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              |||||| |||
Db         10 GGCCAATGTC 1


RESULT 115
AAF42385
ID   AAF42385 standard; DNA; 10 BP.
XX
AC   AAF42385;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9124.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis
PT   of gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle -
```

```
XX
PS   Example; Page 325; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
CC   progression comprising contacting human DNA with a probe which comprises
CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC   member of a class of drugs having a characteristic effect on gene
CC   expression in a yeast cell comprising contacting a yeast cell with a
CC   candidate drug and monitoring expression in the yeast cell of at least 1
CC   NORF gene whose expression is affected by the class of drugs. The NORF
CC   genes may be used to study, monitor and affect phases of the cell cycle,
CC   the differentially expressed genes may be used as markers of phases of
CC   the cell cycle. The methods may be used to identify candidate drugs which
CC   affect the cell cycle and for identification of antifungal drugs.
CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC   primers used in the SAGE method, in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 4 A; 3 C; 3 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||| |||
Db          1 GCCAGGACAA 10


RESULT 116
AAF43779/c
ID   AAF43779 standard; DNA; 10 BP.
XX
AC   AAF43779;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11918.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis
PT   of gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle -
XX
PS   Example; Page 375; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
CC   progression comprising contacting human DNA with a probe which comprises
CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC   member of a class of drugs having a characteristic effect on gene
CC   expression in a yeast cell comprising contacting a yeast cell with a
CC   candidate drug and monitoring expression in the yeast cell of at least 1
CC   NORF gene whose expression is affected by the class of drugs. The NORF
CC   genes may be used to study, monitor and affect phases of the cell cycle,
CC   the differentially expressed genes may be used as markers of phases of
CC   the cell cycle. The methods may be used to identify candidate drugs which
CC   affect the cell cycle and for identification of antifungal drugs.
CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC   primers used in the SAGE method, in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              || |||||||
Db         10 GCGAGGCCAA 1


RESULT 117
ABV84222
ID   ABV84222 standard; cDNA; 10 BP.
XX
AC   ABV84222;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human heat shock protein 40 (HSP40-1) SAGE tag #32.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-0012328.
XX
PR   19-JAN-2001; 2001JP-0012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
```

```
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes -
XX
PS   Claim 1; Page 10; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis
CC   C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC   of the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84191-ABV84290 are SAGE tags representing the 100 most highly
CC   expressed genes out of those genes which are overexpressed in chronic
CC   hepatitis C liver tissue compared with normal liver tissue.
XX
SQ   Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10


RESULT 118
ABV84641/c
ID   ABV84641 standard; cDNA; 10 BP.
XX
AC   ABV84641;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human HCC/chronic hepatitis C differentially expressed EST SAGE tag #451.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; EST; expressed sequence tag;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-0012328.
XX
PR   19-JAN-2001; 2001JP-0012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes -
XX
PS   Claim 37; Page 23; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis
CC   C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC   of the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84591-ABV84690 are SAGE tags representing the 100 most highly
CC   expressed genes out of those genes which are overexpressed in
CC   hepatocellular carcinoma compared with chronic hepatitis C liver tissue.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              ||||||||.|
Db         10 AGGCCAAACT 1


RESULT 119
ABV84947/c
ID   ABV84947 standard; cDNA; 10 BP.
XX
AC   ABV84947;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human multiple HCC highly expressed genes SAGE tag #757.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-0012328.
XX
PR   19-JAN-2001; 2001JP-0012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes -
XX
PS   Claim 64; Page 31; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
```

```
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis
CC   C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC   of the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC   expressed in hepatocellular carcinoma.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 120
ABV78373/c
ID   ABV78373 standard; cDNA; 10 BP.
XX
AC   ABV78373;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human Th2 cell SAGE tag, SEQ ID NO:84.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th2 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   immune disorder; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002186482-A.
XX
PD   02-JUL-2002.
XX
PF   19-DEC-2000; 2000JP-0385816.
XX
PR   19-DEC-2000; 2000JP-0385816.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-594261/64.
XX
PT   Human activated Th1 and Th2 cell expression gene group, useful for the
PT   diagnosis and treatment of Th1 and Th2-related diseases -
XX
PS   Claim 10; Page 9; 60pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are expressed in activated human Th1
CC   and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC   of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC   lying nearest to the polyA region of cDNAs derived from a variety of
CC   genes. These tags serve to uniquely identify each transcript and can thus
CC   be used to analyse the pattern of gene expression in particular cell
CC   types. The invention also relates to proteins encoded by the genes
CC   expressed in Th1 and/or Th2 cells, antibodies against these proteins,
CC   and inhibitors of the expression of groups of genes that are expressed
CC   in either or both the two cell types. Groups of genes expressed in Th1
CC   and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC   and Th2-related disorders. Sequences ABV78340-ABV78389 are SAGE tags
CC   representing 50 genes which are most highly expressed in Th2 cells.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 121
ABK95837
ID   ABK95837 standard; DNA; 10 BP.
XX
AC   ABK95837;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #8.
XX
KW   Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KW   glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KW   amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO200244198-A2.
XX
PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-US44781.
XX
PR   30-NOV-2000; 2000US-250254P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Kazemi A,  Russo DP,  Sausker EA;
XX
DR   WPI; 2002-519580/55.
XX
PT   Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT   Amino Acid Transporter), Member 4 isogenes, for improving efficiency
PT   and reliability in drug development for treating cancers -
XX
PS   Claim 17; Page 16; 139pp; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising a
CC   first nucleotide sequence which comprises solute carrier family 1
CC   (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
CC   (II) and an isolated polypeptide (III) comprising an amino acid sequence
CC   which is a polymorphic variant of a reference sequence for SLC1A4
CC   protein. Also described are methods for: (1) haplotyping or genotyping
CC   SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
CC   gene of an individual; (3) identifying an association between a trait and
CC   at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful
CC   in screening for drugs targeting (III) that are useful for treating
CC   cancer, neurological diseases and amino acid transporter disorders. The
CC   methods are useful for improving the efficiency and reliability of
CC   several steps in the discovery and development of drugs for treating
CC   diseases associated with SLC1A4 activity. The haplotyping method is also
CC   used by the pharmaceutical research scientist to validate SLC1A4 as a
CC   candidate target for treating a specific condition or disease predicted
CC   to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
CC   and amino acid transporter disorders, and in the design of clinical
CC   trials for treating a specific condition of disease associated with
CC   SLC1A4 activity. The methods are also useful for screening compounds
CC   targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
CC   prognostic and therapeutic methods. ABK95761-ABK95877 represent
CC   SLC1A4 gene allele-specific oligonucleotides, primer extension
CC   oligonucleotides and related PCR primers used to identify single
CC   nucleotide polymorphisms (SNP) of the gene.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 other;
```

```
  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              ||||||| ||
Db          1 CCGGGCCTGG 10
```

RESULT 122
ABK95838
ID ABK95838 standard; DNA; 10 BP.
XX
AC ABK95838;
XX
DT 24-SEP-2002 (first entry)
XX
DE Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #9.
XX
KW Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KW glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KW amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO200244198-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US44781.
XX
PR 30-NOV-2000; 2000US-250254P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Kazemi A, Russo DP, Sausker EA;
XX
DR WPI; 2002-519580/55.
XX
PT Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency
PT and reliability in drug development for treating cancers -
XX
PS Claim 17; Page 16; 139pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC first nucleotide sequence which comprises solute carrier family 1
CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
CC which is a polymorphic variant of a reference sequence for SLC1A4
CC protein. Also described are methods for: (1) haplotyping or genotyping
CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
CC gene of an individual; (3) identifying an association between a trait and
CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful
CC in screening for drugs targeting (III) that are useful for treating
CC cancer, neurological diseases and amino acid transporter disorders. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with SLC1A4 activity. The haplotyping method is also
CC used by the pharmaceutical research scientist to validate SLC1A4 as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
CC and amino acid transporter disorders, and in the design of clinical
CC trials for treating a specific condition of disease associated with
CC SLC1A4 activity. The methods are also useful for screening compounds
CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
CC prognostic and therapeutic methods. ABK95761-ABK95877 represent
CC SLC1A4 gene allele-specific oligonucleotides, primer extension
CC oligonucleotides and related PCR primers used to identify single
CC nucleotide polymorphisms (SNP) of the gene.
XX
SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 U; 0 other;

```
  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db          1 GCGCCAGGCC 10
```

RESULT 123
ABA97040/c
ID ABA97040 standard; DNA; 10 BP.
XX
AC ABA97040;
XX
DT 18-JUN-2002 (first entry)
XX
DE ZFP36 extension primer for detecting polymorphisms SEQ ID 41.
XX
KW Polymorphic variant; ZFP36; immunosuppressive; antirheumatic;
KW antiarthritic; drug screening; isogene; haplotype pair;
KW autoimmune disease; rheumatoid arthritis; haplotyping; genotyping;
KW allele specific oligonucleotide; ASO; single nucleotide polymorphism;
KW SNP; zinc finger protein; mouse zfp-36; ss; gene therapy; transgenic;
KW primer.
XX
OS Homo sapiens.
XX
PN WO200179226-A2.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2001; 2001WO-US12254.
XX
PR 13-APR-2000; 2000US-196602P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kliem SE, Koshy B, Parks KE;
XX
DR WPI; 2002-075059/10.
XX
PT Novel polymorphic variants of zinc finger protein homologous to zfp-36
PT in mouse gene, useful in studying expression and function of the
PT protein, useful for screening drugs to treat diseases e.g. rheumatoid
PT arthritis -
XX
PS Claim 18; Page 14; 60pp; English.
XX
CC The present sequence is that of an oligonucleotide used for assaying a
CC polymorphism in the zinc finger protein homologous to zfp-36 in mouse
CC (ZFP36) gene of the invention. The specification describes a newly
CC isolated polynucleotide comprising a sequence which is a polymorphic
CC variant (PV) of a reference sequence for the ZFP36 gene (see ABA97001) or
CC its fragment and its encoded protein. The ZFP36 polynucleotides and
CC polypeptides have antirheumatic, immunosuppressive and antiarthritic
CC activities. The ZFP36 polypeptide is useful for screening drugs targeting
CC the ZFP36 polypeptide. ZFP36 isogenes or haplotype pairs are useful for
CC improving the efficiency and reliability of the discovery and development
CC of drugs for treating diseases associated with ZFP36 activity, e.g.,
CC autoimmune diseases such as rheumatoid arthritis. Haplotyping the ZFP36
CC gene in an individual gives useful information for validating ZFP36 as a
CC candidate target for treating a specific condition predicted to be
CC associated with ZFP36 activity. Genotyping the ZFP36 gene of an
CC individual can give information used for developing diagnostic tests and
CC therapeutic treatments. The isolated polynucleotide is useful in studying
CC the expression and function of ZFP36 and in drug screening. Antibodies
CC specific for the ZFP36 protein are useful in many diagnostic and
CC prognostic formats and therapeutic methods. A recombinant non-human
CC organism transformed with the ZFP36 gene is useful in studying expression
CC of the ZFP36 isogenes in vivo, for in vivo drug screening and testing.
CC Allele-specific oligonucleotides (ASO) are useful as probes and primers
CC and for assaying a polymorphism in the target region.

```
XX
SQ   Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||||||
Db         10 CCGGCCAGGC 1


RESULT 124
ABK64054/c
ID   ABK64054 standard; DNA; 10 BP.
XX
AC   ABK64054;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human BF gene allele-specific oligonucleotide PCR primer #5.
XX
KW   Human; B-factor; properdin; BF; primer; ss; gene therapy; drug screening;
KW   antidiabetic; dermatological; diabetes; immunosuppressive;
KW   antiinflammatory; systemic lupus erythematosus.
XX
OS   Homo sapiens.
XX
PN   WO200218414-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US27098.
XX
PR   29-AUG-2000; 2000US-228940P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Finkel K,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-304244/34.
XX
PT   New genetic variants having polymorphisms in the B-Factor, Properdin
PT   (BF) gene, useful for studying the function of BF, and for treating
PT   disorders affected by expression or function of the BF isogene  -
XX
PS   Claim 19; Page 16; 151pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding the human B-factor properdin protein (BF). A method for
CC   haplotyping the BF gene in an individual comprises identifying the
CC   nucleotide at one or more polymorphic sites and determining whether one
CC   of the copies of the gene is defined by one of the BF haplotypes given in
CC   the specification or whether both copies are defined by a haplotype pair.
CC   This method is useful in genotyping, whereby all possible haplotype pairs
CC   can be assigned to specific genotypes. An association between a trait and
CC   a haplotype or haplotype pair of the BF gene can be identified by
CC   comparing the frequency of the haplotype or haplotype pair in a
CC   population exhibiting the trait with the frequency of the haplotype or
CC   haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. BF and its corresponding DNA are used
CC   for studying the expression and function of BF, for use in screening for
CC   candidate drugs to treat diseases related to BF activity, such as
CC   diabetes and systemic lupus erythematosus. Sequences ABK64050-ABK64105
CC   represent allele-specific PCR primers used to detect human BF gene
CC   polymorphisms.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              ||||||||  |
Db         10 GGCCAAAGAC 1


RESULT 125
AAS19876
ID   AAS19876 standard; DNA; 10 BP.
XX
AC   AAS19876;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Oligonucleotide #56 to detect human RANGAP1 gene polymorphisms.
XX
KW   Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KW   chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW   cancer; irregular cell cycle associated disorder; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179240-A2.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-US12455.
XX
PR   17-APR-2000; 2000US-198072P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-075068/10.
XX
PT   Genotyping human Ran GTPase activating protein 1 gene of individual for
PT   determining haplotype of individual, involves determining identity of
PT   nucleotide pair at specific polymorphic sites for two copies of the
PT   gene  -
XX
PS   Claim 17; Page 16; 148pp; English.
XX
CC   The present invention relates to novel single nucleotide polymorphisms
CC   (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC   located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC   genotyping the RANGAP1 gene. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC   primer-extension oligonucleotides for detecting the RANGAP1 gene
CC   polymorphisms. The polynucleotides and screened compounds are useful for
CC   treatment of diseases associated with RANGAP1 activity, such as
CC   cancer and other disorders associated with an irregular cell cycle.
CC   AAS19821-AAS19898 represent primer-extension oligonucleotides for
CC   detecting human RANGAP1 gene polymorphisms.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              ||||||| ||
Db          1 GGCCAGGACA 10


RESULT 126
ABK23567/c
ID   ABK23567 standard; DNA; 10 BP.
XX
AC   ABK23567;
XX
DT   09-APR-2002  (first entry)
```

XX
DE Transcript tag DNA sequence #156 induced or suppressed by N-myc.
XX
KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS Homo sapiens.
XX
PN WO200185941-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-NL00361.
XX
PR 11-MAY-2000; 2000EP-0201698.
PR 29-JUN-2000; 2000EP-0202284.
XX
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI Versteeg R, Caron HN;
XX
DR WPI; 2002-066603/09.
XX
PT A new nucleic acid library of myc-dependent downstream genes capable of
PT supporting a neoplastic characteristic of cancer is useful to find new
PT therapies and diagnoses for cancer -
XX
PS Disclosure; Page 53; 69pp; English.
XX
CC The present invention relates to a nucleic acid library comprising
CC myc-dependent downstream genes or their functional fragments essentially
CC capable of supporting a neoplastic character of cancer such as growth,
CC invasion or spread. These myc target or tag sequences are identified
CC by SAGE (serial analysis of gene expression). The library is useful to
CC find new diagnoses and treatments for cancer. The invention is also
CC useful to enhance production of recombinant proteins in a production
CC system with high expression of endogenous or transfected myc oncogenes.
CC ABK23412-ABK23828 represent transcript tag DNA sequences that are
CC activated or repressed by N-myc in human neuroblastoma.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCA 15
|| |||||||
Db 10 GGGCAGGCCA 1

RESULT 127
ABK24232
ID ABK24232 standard; DNA; 10 BP.
XX
AC ABK24232;
XX
DT 09-APR-2002 (first entry)
XX
DE Retinaldehyde-binding protein 1 ASO primer extension primer #5.
XX
KW Human; retinaldehyde-binding protein 1; ss; RLBP1; haplotype; primer;
KW genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR;
KW chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.
XX
OS Homo sapiens.
XX
PN WO200192278-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US17252.
XX
PR 26-MAY-2000; 2000US-207618P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kazemi A, Koshy B;
XX
DR WPI; 2002-122053/16.
XX
PT New genetic variants having polymorphisms in the retinaldehyde-binding
PT protein 1 gene, useful for studying the function of and for expressing
PT RLBP1 protein for use in screening drugs for treating diseases related
PT to RLBP1 activity -
XX
PS Claim 18; Page 14; 107pp; English.
XX
CC The invention relates to an isolated polynucleotide, which comprises
CC genes and haplotypes of the retinaldehyde-binding protein 1 (RLBP1) gene.
CC The polynucleotide comprises polymorphic sites in the RLBP1 gene, which
CC are referred to as PS1-24 to designate the order in which they are
CC located in the gene. Also included are methods for haplotyping or
CC genotyping the RLBP1 gene of an individual, a method for predicting a
CC haplotype pair for the RLBP1 gene of an individual, a method for
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of the RLBP1 gene, a composition comprising at least one
CC genotyping oligonucleotide for detecting a polymorphism in the RLBP1 gene
CC at a PS consisting of PS1-PS24, a kit for genotyping the RLBP1 gene of an
CC individual comprising a set of oligonucleotides designed to genotype each
CC of PS1-PS24 recombinant non-human organisms transformed or transfected
CC with the isolated polynucleotide, where the organism expresses a RLBP1
CC protein encoded by the first nucleotide sequence or expresses an RLBP1
CC protein encoded by the polymorphic variant sequence, an isolated
CC polypeptide comprising an amino acid sequence that is a polymorphic
CC variant of a reference sequence for the RLBP1 protein or its fragment,
CC an anti-RLBP1 antibody, a method for screening for drugs targeting the
CC isolated polypeptide, and a computer system for storing and analysing
CC polymorphism data for the RLBP1 oncogene gene.
CC The polynucleotide comprising polymorphisms in the RLBP1 gene is
CC useful in studying the expression and function of RLBP1, and in
CC expressing RLBP1 protein for use in screening candidate drugs to treat
CC diseases related to RLBP1 activity (e.g autosomal recessive
CC retinitis pigmentosa (arRP). The methods and haplotypes are
CC useful in improving the efficiency and output of several steps in the
CC drug discovery and development process, including target validation,
CC identifying lead compounds, and early phase clinical trials. These are
CC also useful for designing clinical trials of candidate drugs for
CC treating a specific condition or disease, as well as for screening
CC compounds targeting RLBP1 to treat a specific condition or disease
CC predicted to be associated with RLBP1 activity. The kit and method are
CC useful for determining whether an individual has one of the haplotypes
CC or haplotype pairs cited above. The transgenic animals are useful for
CC studying expression of the RLBP1 isogenes in vivo, for in vivo
CC screening and testing of drugs targeted against RLBP1 protein, and for
CC testing the efficacy of therapeutic agents and compounds for retinal
CC diseases in a biological system. The gene for RLBP1 is located on
CC chromosome 15q26. The present sequence is an allele specific
CC oligonucleotide (ASO) PCR primer for amplifying a nucleic acid containing
CC a polymorphic RLBP sequence, using the primer extension method.
XX
SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 U; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCAGGCCAAA 17
|||||||| |
Db 1 CCAGGCCAGA 10

RESULT 128
AAS99275
ID AAS99275 standard; DNA; 10 BP.

XX
AC AAS99275;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human F12 gene allele-specific oligonucleotide PCR primer #2.
XX
KW Human; coagulation factor XII; F12; haplotyping; haplotype pair; ss;
KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;
KW coronary artery disease; liver disease; spontaneous abortion; cardiant;
KW Alzheimer's disease; blood coagulation; hepatotropic; neuroprotective;
KW nootropic; coagulant; antiabortive; sequencing primer; PCR primer; probe;
KW primer tail.
XX
OS Homo sapiens.
XX
PN WO200179228-A2.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2001; 2001WO-US12257.
XX
PR 14-APR-2000; 2000US-197837P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Nandabalan K;
XX
DR WPI; 2002-075061/10.
XX
PT Novel isolated human coagulation factor XII polynucleotide, F12 useful
PT for treatment of e.g. coronary artery disease, comprises a sequence
PT which is a polymorphic variant of a reference sequence for F12 gene or
PT its fragment -
XX
PS Claim 18; Page 14; 72pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human coagulation factor XII (F12) polypeptide. A method for
CC haplotyping the F12 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the F12 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the F12 gene can be identified
CC by comparing the frequency of the haplotype or haplotype pair in a
CC population exhibiting the trait with the frequency of the haplotype or
CC haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. F12 and its corresponding DNA are used
CC for studying the expression and function of F12, for use in screening for
CC candidate drugs to treat disorders related to F12 activity such as
CC coronary artery disease, liver disease, spontaneous abortion, Alzheimer's
CC disease and other diseases associated with defects in blood coagulation.
CC The sequences are also useful for studying the effect of variation on the
CC biological activity of F12 as well as on the binding affinity of
CC candidate drugs targeting F12. Sequences AAS99229-AAS99305 represent
CC probes, primers and primer tails used to detect F12 gene polymorphisms.
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAG 18
              | ||||||||
Db          1 CTGGCCAAAG 10
```

RESULT 129
AAS16750/c
ID AAS16750 standard; DNA; 10 BP.
XX
AC AAS16750;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human APOA4 ASO, primer extension primer #3 terminal sequence.
XX
KW Human; ss; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
KW atherosclerosis; PCR primer; primer extension.
XX
OS Homo sapiens.
XX
PN WO200177124-A2.
XX
PD 18-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10670.
XX
PR 05-APR-2000; 2000US-194362P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;
XX
DR WPI; 2002-041281/05.
XX
PT New haplotypes of the human apolipoprotein A-IV gene, useful to
PT diagnose and treat disorders associated with its abnormal expression or
PT function such as coronary artery disease -
XX
PS Claim 17; Page 15; 71pp; English.
XX
CC The invention relates to haplotyping the human apolipoprotein A-IV
CC (APOA4) gene of an individual, comprising determining if the individual
CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
CC specification. Also disclosed are genotyping oligonucleotides (or
CC allele specific oligonucleotides, ASO) as well as methods for correlating
CC a particular haplotype pair with a trait e.g. obesity, in a population.
CC The APOA4 gene is located on chromosome 11q23-qter. The methods of the
CC invention are useful to diagnose and develop treatment for disorders
CC associated with abnormal APOA4 expression or function, for example
CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
CC screened compounds are useful for the treatment of disorders associated
CC with abnormal APOA4 expression or function such as coronary artery
CC disease. The present sequence is the terminus of an APOA4 allele specific
CC oligonucleotide, ASO, primer extension PCR primer used to detect an APOA4
CC polymorphism.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              | ||||||||
Db         10 CAGGGCCAGG 1
```

RESULT 130
ABL42671/c
ID ABL42671 standard; cDNA; 10 BP.
XX
AC ABL42671;
XX
DT 12-APR-2002 (first entry)
XX
DE Human maturation/activation dendritic cell expression gene tag #45.
XX
KW Human; maturation/activation dendritic cell expression gene; tag;
KW maturation; activation; dendritic cell; ss.

```
XX
OS   Homo sapiens.
XX
PN   JP2001327293-A.
XX
PD   27-NOV-2001.
XX
PF   22-MAY-2000; 2000JP-0150562.
XX
PR   22-MAY-2000; 2000JP-0150562.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-127070/17.
XX
PT   Human maturation/activation dendritic cell expression gene group -
XX
PS   Claim 1; Page 9; 41pp; Japanese.
XX
CC   The present invention describes a human maturation/activation dendritic
CC   cell (DC) expression gene group consisting of 100 genes which show the
CC   highest expression among the genes expressed in human maturation/
CC   activation DC. Also described are: (1) a protein expressed by the above
CC   human maturation/activation DC expression gene; (2) an antibody against
CC   the protein; and (3) an antagonist against the expression of each gene
CC   belonging to the above gene group. The gene group is useful for the
CC   treatment and the diagnosis of various human diseases related to human
CC   DC. ABL42627 to ABL42926 represent specifically claimed human
CC   maturation/activation DC expression gene tags from the present invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 87;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 131
ABV62380
ID   ABV62380 standard; cDNA; 11 BP.
XX
AC   ABV62380;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 166.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 30; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || |||||||
Db          2 CCTGGCCAGG 11


RESULT 132
ABV69801
ID   ABV69801 standard; cDNA; 11 BP.
XX
AC   ABV69801;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7587.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Claim 24; Page 240; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
```

```
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || |||||||
Db          2 CCTGGCCAGG 11


RESULT 133
AAX54916
ID   AAX54916 standard; DNA; 11 BP.
XX
AC   AAX54916;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 68; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 11 BP; 0 A; 4 C; 6 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              |||||| |||
Db          2 CGGGCCGGGC 11


RESULT 134
AAF20485
ID   AAF20485 standard; DNA; 11 BP.
XX
AC   AAF20485;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2052.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 262; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
```

CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 11 BP; 0 A; 4 C; 6 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGGGCCAGGC 13
||||||.|||
Db 2 CGGGCCGGGC 11

RESULT 135
AAA34363
ID AAA34363 standard; DNA; 11 BP.
XX
AC AAA34363;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2052.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 523; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 11 BP; 0 A; 4 C; 6 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGGGCCAGGC 13
||||||.|||
Db 2 CGGGCCGGGC 11

RESULT 136
AAZ59919/c
ID AAZ59919 standard; DNA; 11 BP.
XX
AC AAZ59919;
XX
DT 08-MAY-2000 (first entry)
XX
DE COUP-TF inverted repeat binding site.
XX
KW COUP-TF binding site; inverted repeat; minimal packaging element;
KW adenovirus; chicken ovalbumin upstream promoter transcription factor;
KW repressor binding site; DNA delivery; recombinant virus; ds.
XX
OS Mastadenovirus.
XX
PN WO9953085-A2.
XX
PD 21-OCT-1999.
XX
PF 15-APR-1999; 99WO-US08294.
XX
PR 15-APR-1998; 98US-0081867.
PR 05-JUN-1998; 98US-0088321.
XX
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
XX
PI Hearing P, Schmid SI, Ostapchuk PH, Erturk E;
XX
DR WPI; 2000-052657/04.
XX
PT Regulating adenoviral packaging by incorporation of repressor binding
PT sites that allow selective suppression of packaging, used for gene
PT therapy -
XX
PS Example 5; Page 39; 71pp; English.
XX
CC The invention relates to the regulation of adenoviral packaging.

CC The method of the invention comprises propagating an adenoviral
CC vector containing a repressor binding site, in the absence of the
CC repressor. After propagation, vector packaging is repressed by the
CC appropriate repressor protein. The invention also encompasses an
CC adenoviral vector that includes an adenoviral packaging sequence
CC containing several COUP-TF (chicken ovalbumin upstream promoter
CC transcription factor) binding sites (AAZ59919). Adenoviral vectors
CC containing repressor binding sites are used for DNA delivery, e.g., for
CC expression of a therapeutic protein; in genetic immunisation; or to
CC produce antiviral DNA or antisense RNA. Typical heterologous genes that
CC can be expressed include those for interleukin-2, alpha1-antitrypsin,
CC cystic fibrosis transmembrane conductance regulator and coagulation
CC factor VIII. These vectors have very large capacity (up to 36 kb) for
CC foreign DNA and minimise the risk of generating replication competent
CC virus (since vector and helper virus can be designed such that they
CC have no overlapping packaging sequences that might permit homologous
CC recombination). The presence of the repressor binding site allows
CC selective inhibition of virion production (i.e., packaging of one vector
CC in the presence of another). The present sequence represents a COUP-TF
CC inverted repeat binding site. COUP-TF binds to the consensus sequence
CC 5'-GGTCA-3' when situated as a direct or inverted repeat. These binding
CC sites overlap the A repeat AVI sequence, with other A repeats contain
CC similar sequenec motifs. Binding of COUP-TF can specifically repress
CC adenovirus packaging.
XX
SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GGCCAAAGTC 20
               || |||||||
Db          11 GGTCAAAGTC 2
```

RESULT 137
ABQ81854
ID ABQ81854 standard; DNA; 11 BP.
XX
AC ABQ81854;
XX
DT 19-NOV-2002 (first entry)
XX
DE Kaposi's Sarcoma SAGE library Tag No.4 SEQ ID NO:4.
XX
KW Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss.
XX
OS Homo sapiens.
XX
PN EP1225233-A2.
XX
PD 24-JUL-2002.
XX
PF 23-JAN-2002; 2002EP-0075264.
XX
PR 23-JAN-2001; 2001EP-0200228.
PR 28-SEP-2001; 2001EP-0203703.
PR 28-SEP-2001; 2001US-325722P.
XX
PA (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
PI Van Der Kuyl AC, Cornelissen M;
XX
DR WPI; 2002-668396/72.
XX
PT Determining presence of a tumor cell or angiogenesis, and the
PT effectiveness of treatment, by detecting the presence of marker genes
PT is useful to detect and monitor treatment of Kaposi's Sarcoma -
XX
PS Claim 12; Page 8; 38pp; English.
XX
CC The present invention describes a method for determining if an individual
CC has a tumour cell or site of angiogenesis, or if a treatment is effective
CC in changing angiogenesis or changing a status of a set of target cells,
CC comprising determining if a sample of the subject has an expression
CC product of at least one marker gene. Also described is a compound capable
CC of altering the expression or activity of Keratin 14, TIE 1, Salioadhesin
CC or Siglec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed
CC Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from
CC the present invention can be used in a diagnostic method, particularly as
CC an indicator of angiogenesis or to determine presence of a tumour cell.
CC The method of the invention is suitable to determine within a few days if
CC a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to
CC ABQ82006 represent nucleotide sequence used in the exemplification of the
CC present invention.
XX
SQ Sequence 11 BP; 3 A; 4 C; 4 G; 0 U; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GGCCAAAGTC 20
               ||||||| |
Db           1 GGCCAAAGGC 10
```

RESULT 138
ABV62551/c
ID ABV62551 standard; cDNA; 11 BP.
XX
AC ABV62551;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 337.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 35; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.

```
XX
SQ   Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 139
ABV62704
ID   ABV62704 standard; cDNA; 11 BP.
XX
AC   ABV62704;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 490.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 39; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              || |||||||
Db          1 GGCCCAGGCC 10


RESULT 140
ABV63037
ID   ABV63037 standard; cDNA; 11 BP.
XX
AC   ABV63037;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 823.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 48; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              || |||||||
Db          1 CCTGGCCAAA 10


RESULT 141
ABV65097
ID   ABV65097 standard; cDNA; 11 BP.
XX
AC   ABV65097;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2883.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 105; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis;.scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||||||
Db          1 CTGGCCAGGC 10


RESULT 142
ABV65146
ID   ABV65146 standard; cDNA; 11 BP.
XX
AC   ABV65146;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2932.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 106; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 2 A; 4 C; 5 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db          2 GAGCCAGGCC 11


RESULT 143
ABV65638/c
ID   ABV65638 standard; cDNA; 11 BP.
XX
AC   ABV65638;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3424.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 120; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
```

```
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              ||||||| ||
Db         10 GGCCAAACTC 1


RESULT 144
ABV65978
ID   ABV65978 standard; cDNA; 11 BP.
XX
AC   ABV65978;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3764.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 129; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10


RESULT 145
ABV66142/c
ID   ABV66142 standard; cDNA; 11 BP.
XX
AC   ABV66142;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3928.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 134; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              ||||| ||||
Db         10 GGCCAGAGTC 1


RESULT 146
ABV66964/c
ID   ABV66964 standard; cDNA; 11 BP.
XX
AC   ABV66964;
XX
```

```
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4750.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 156; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCCGGCCAA 1


RESULT 147
ABV67427/c
ID   ABV67427 standard; cDNA; 11 BP.
XX
AC   ABV67427;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5213.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 169; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              || |||||||
Db         11 GGCCCAGGCC 2


RESULT 148
ABV67547
ID   ABV67547 standard; cDNA; 11 BP.
XX
AC   ABV67547;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5333.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
```

```
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 172; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              ||||| ||||
Db          2 AGGCCCAAGT 11


RESULT 149
ABV68518/c
ID   ABV68518 standard; cDNA; 11 BP.
XX
AC   ABV68518;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6304.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 200; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              || |||||||
Db         10 TCGGGGCCAG 1


RESULT 150
ABV68762/c
ID   ABV68762 standard; cDNA; 11 BP.
XX
AC   ABV68762;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6548.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 207; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1
```

```
RESULT 151
ABV69053
ID   ABV69053 standard; cDNA; 11 BP.
XX
AC   ABV69053;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6839.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 215; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 3 A; 4 C; 4 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GGCCAAAGTC 20
               |||||||| |
Db           1 GGCCAAAGGC 10


RESULT 152
ABV69138/c
ID   ABV69138 standard; cDNA; 11 BP.
XX
AC   ABV69138;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6924.
XX.
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 217; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 GCCAGGCCAA 16
               |||||||| |
Db          11 GCCAGGCCCA 2


RESULT 153
ABV69411/c
ID   ABV69411 standard; cDNA; 11 BP.
XX
AC   ABV69411;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7197.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
```

```
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 226; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||||| |
Db         10 GCCAGGCCCA 1


RESULT 154
ABV69528/c
ID   ABV69528 standard; cDNA; 11 BP.
XX
AC   ABV69528;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7314.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 229; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||||||| ||
Db         10 GGGCCAGTCC 1


RESULT 155
ABV69972/c
ID   ABV69972 standard; cDNA; 11 BP.
XX
AC   ABV69972;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7758.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Claim 24; Page 247; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 156
ABV70125
ID   ABV70125 standard; cDNA; 11 BP.
XX
AC   ABV70125;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7911.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Claim 24; Page 252; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              || |||||||
Db          1 GGCCCAGGCC 10


RESULT 157
ABV70458
ID   ABV70458 standard; cDNA; 11 BP.
XX
AC   ABV70458;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8244.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Claim 24; Page 264; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              || |||||||
Db          1 CCTGGCCAAA 10


RESULT 158
ABQ86459
ID   ABQ86459 standard; cDNA; 11 BP.
XX
AC   ABQ86459;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 214.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
```

```
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15178.
XX
PR   03-JAN-2001; 2001DE-1000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and ageing, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential
PT   gene expression  -
XX
PS   Claim 8; Page 45; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              ||||| ||||
Db          2 AGGCCCAAGT 11


RESULT 159
ABQ86573/c
ID   ABQ86573 standard; cDNA; 11 BP.
XX
AC   ABQ86573;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 328.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15178.
XX
PR   03-JAN-2001; 2001DE-1000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and ageing, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential
PT   gene expression  -
XX
PS   Claim 8; Page 50; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ   Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              |||||||| |
Db         11 GCCAGGCCCA 2


RESULT 160
ABQ87161
ID   ABQ87161 standard; cDNA; 11 BP.
XX
AC   ABQ87161;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 916.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15178.
XX
PR   03-JAN-2001; 2001DE-1000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and ageing, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential
PT   gene expression  -
XX
PS   Claim 8; Page 75; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ   Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              || |||||||
Db          1 CCTGGCCAAA 10


RESULT 161
ABQ87207
ID   ABQ87207 standard; cDNA; 11 BP.
XX
AC   ABQ87207;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 962.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15178.
XX
PR   03-JAN-2001; 2001DE-1000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and ageing, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential
PT   gene expression  -
XX
PS   Claim 8; Page 77; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ   Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10


RESULT 162
ABL92021
ID   ABL92021 standard; cDNA; 11 BP.
XX
AC   ABL92021;
XX
DT   30-MAY-2002  (first entry)
XX
DE   Short human Tumour Endothelial Marker SEQ ID NO 119.
XX
KW   Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW   normal endothelial marker; pan-endothelial marker; immunostimulant;
KW   antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW   polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW   psoriasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200210217-A2.
XX
PD   07-FEB-2002.
XX
PF   01-AUG-2001; 2001WO-US24031.
XX
PR   02-AUG-2000; 2000US-222599P.
PR   11-AUG-2000; 2000US-224360P.
PR   11-APR-2001; 2001US-282850P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   St Croix B,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2002-291856/33.
XX
PT   An isolated molecule comprising an antibody variable region which
PT   specifically binds to an extracellular domain of a tumor endothelial
PT   marker (TEM) protein, useful for inhibiting tumor growth -
XX
PS   Example 5; Page 22; 331pp; English.
XX
CC   The invention relates to an isolated molecule comprising an antibody
CC   variable region which specifically binds to an extracellular domain of a
CC   tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC   ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC   proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC   They are useful for inhibiting tumour growth, neoangiogenesis in
CC   subjects bearing a vascularised tumour, polycystic kidney disease,
CC   diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
CC   and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
CC   ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
CC   sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
CC   ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
CC   and pan-endothelial markers (PEM) ABL91903-ABL91995. The present sequence
CC   is that of an oligonucleotide marker useful to the invention.
XX
SQ   Sequence 11 BP; 4 A; 3 C; 3 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGCCCAAAGT 10


RESULT 163
ABX71946
ID   ABX71946 standard; DNA; 11 BP.
XX
AC   ABX71946;
XX
DT   12-MAR-2003  (first entry)
XX
DE   DNA tag used to identify human gene encoding TEM 26.
XX
KW   Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW   Tumour endothelial marker; normal endothelial marker; PEM;
KW   pan-endothelial marker; polycystic kidney disease; psoriasis;
KW   diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
```

```
KW   neoangiogenesis; immune response; cytostatic; antidiabetic;
KW   ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200283874-A2.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-US08253.
XX
PR   11-APR-2001; 2001US-282850P.
PR   06-FEB-2002; 2002US-354262P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Carson-Walter E,  St Croix B,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2003-093016/08.
XX
PT   New purified human transmembrane protein, designated as tumour
PT   endothelial marker (TEM) 3, useful for detecting, diagnosing or
PT   treating tumours, polycystic kidney disease, diabetic retinopathy,
PT   rheumatoid arthritis or psoriasis -
XX
PS   Disclosure; Page 104; 374pp; English.
XX
CC   The present invention relates to a novel method for the isolation of
CC   endothelial cells (ECs), and the identification of genes expressed in
CC   normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC   endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC   identified in human ECs. The human EC marker proteins and the
CC   polynucleotide sequences encoding them are useful for detecting,
CC   diagnosing or treating tumours as well as polycystic kidney disease,
CC   diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are
CC   also useful for inhibiting neoangiogenesis or tumour angiogenesis,
CC   for inducing an immune response to tumour endothelial cells in a
CC   patient, or for identifying candidate drugs for treating tumours.
CC   ABX71828-ABX71999 represent DNA tags for human PEM, TEM or NEM
CC   genes.
XX
SQ   Sequence 11 BP; 4 A; 3 C; 3 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
               || |||||||
Db          1 AGCCCAAAGT 10


RESULT 164
AAA80792
ID   AAA80792 standard; DNA; 8 BP.
XX
AC   AAA80792;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 105.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-0859954.
XX
PR   15-APR-1996;   96US-0632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction
PT   and other primer processes comprises primer walking of octamer
PT   oligonucleotides -
XX
PS   Example 8; Column 77-78; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and
CC   corresponding complementary sequences, where the library primer is
CC   complementary to a known sequence adjacent to the unknown sequence or
CC   is complementary to a sequence in a known extension product. The method
CC   is useful for DNA nucleotide sequencing, in PCR, and in other processes
CC   which make use of primers.  The octamers are used to identify coding
CC   sequences. Primer walking using the octamer libraries is advantageous
CC   over other sequencing methods because it does not require multiple
CC   cloning steps nor subsequent template preparations, and it is a
CC   directed and methodical approach. AAA80688-A81253 represent the octamer
CC   primers used in the primer walking method of the invention.
XX
SQ   Sequence 8 BP; 3 A; 2 C; 2 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAGT 19
              ||||||||
Db          1 GCCAAAGT 8


RESULT 165
AAV63091/c
ID   AAV63091 standard; cDNA; 9 BP.
XX
AC   AAV63091;
XX
DT   25-JAN-1999  (first entry)
XX
DE   Human Tcf mutant DNA motif.
XX
KW   Tcf; beta-catenin; human; drug; familial adenomatous polyposis; FAP;
KW   cancer; adenomatous polyposis coli; APC; neoplastic; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841631-A2.
XX
PD   24-SEP-1998.
XX
PF   20-MAR-1998;   98WO-US05506.
XX
PR   20-MAR-1997;   97US-0821355.
XX
PA   (UYUT-) RIJKSUNIV UTRECHT.
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Barker N,  Clevers H,  Kinzler KW,  Korinek V,  Morin PJ;
PI   Sparks AB,  Vogelstein B;
XX
DR   WPI; 1998-531569/45.
XX
PT   Intron-free DNA encoding Tcf-4 protein - useful for, e.g.
PT   identifying drugs for treating FAP patients, or patients with
PT   increased risk of developing cancer
```

```
XX
PS   Example 2; Page 14; 58pp; English.
XX
CC   This sequence is a mutant DNA motif from the human Tcf gene family used
CC   in the isolation of novel Tcf proteins. These proteins can be used, along
CC   with beta-catenin in a method of identifying candidate drugs for use
CC   in familial adenomatous polyposis (FAP) patients, or patients with
CC   increased risk of developing cancer. The protein can also be used to
CC   determine the presence or absence in a cell of wild type adenomatous
CC   polyposis coli (APC) gene or a downstream protein in the APC
CC   transcription regulatory pathway. This method involves introducing a
CC   Tcf-responsive reporter gene into the cell, and measuring transcription
CC   of the reporter gene where a cell which supports active transcription of
CC   the reporter gene does not have wild type APC or a downstream protein of
CC   the APC transcription regulatory pathway. The protein can also be used
CC   in a method of diagnosing cancer in a sample suspected of being
CC   neoplastic and for treating a patient with colorectal cancer or other
CC   cancer associated with FAP, comprising administering to the patient a
CC   polypeptide comprising a portion of the APC sequence, comprising the
CC   beta-catenin binding site.
XX
SQ   Sequence 9 BP; 0 A; 4 C; 2 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAG 18
              ||||||||
Db          9 GGCCAAAG 2


RESULT 166
AAX99683/c
ID   AAX99683 standard; DNA; 9 BP.
XX
AC   AAX99683;
XX
DT   05-OCT-1999  (first entry)
XX
DE   Tcf optimal response element mutated sequence.
XX
KW   Mammalian; transcription factor; Tcf-3; Tcf-4; beta-catenin; mouse;
KW   binding domain; Wnt signalling; Wnt/Wingless cascade; anticancer drug;
KW   transactivation; fetal cancer; testis cancer; ovary teratoma; mammary;
KW   myeloblastoma; medulloblastoma; intestinal cancer; response element; ss.
XX
OS   Synthetic.
XX
PN   EP939122-A1.
XX
PD   01-SEP-1999.
XX
PF   27-FEB-1998;   98EP-0200621.
XX
PR   27-FEB-1998;   98EP-0200621.
XX
PA   (UYUT-) RIJKSUNIV UTRECHT.
XX
DR   WPI; 1999-471050/40.
XX
PT   New mouse transcription factors, useful for diagnosing and treating
PT   cancers and screening for anticancer drugs
XX
PS   Disclosure; Page 4; 56pp; English.
XX
CC   The invention relates to mammalian transcription factors Tcf-3 or Tcf-4
CC   protein or their derivatives. The Tcf proteins of the invention comprise
CC   a beta-catenin binding domain and are capable of complexing with beta-
CC   catenin in response to signaling through the Wnt/Wingless cascade. The
CC   Tcf-3 and Tcf-4 genes, proteins and antibodies against the proteins may
CC   be used to screen for candidate anticancer drugs by identifying compounds
CC   which interact with beta-catenin/Tcf-3 or beta-catenin/Tcf-4 complexes
CC   and alter their transactivation activity. Compounds which interact with
CC   the Tcf-3 and Tcf-4 proteins and interfere with their transcriptional
CC   activation, identified using these screens, may be used to treat fetal
CC   cancer, cancers with stem cell phenotypes, testis or ovary teratomas,
CC   myeloblastomas, medulloblastomas, mammary or intestinal cancers. The
CC   present sequence represents a mutated Tcf optimal response element
CC   motif sequence. Mutation of the element abrogates responsiveness.
XX
SQ   Sequence 9 BP; 0 A; 4 C; 2 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAG 18
              ||||||||
Db          9 GGCCAAAG 2


RESULT 167
ABQ72076/c
ID   ABQ72076 standard; DNA; 9 BP.
XX
AC   ABQ72076;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2374.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US43438.
XX
PR   20-NOV-2000; 2000US-0716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering,
PT   comprises first, second and third zinc fingers, ordered from N- to
PT   C-terminus  -
XX
PS   Example 1; Page 61; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
```

CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 0 A; 3 C; 4 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCA 15
||||||·||
Db 9 CCAGGCCA 2

RESULT 168
ABQ72078/c
ID ABQ72078 standard; DNA; 9 BP.
XX
AC ABQ72078;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2376.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 61; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 0 A; 3 C; 4 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCA 15
||||||||
Db 9 CCAGGCCA 2

RESULT 169
ABQ72126/c
ID ABQ72126 standard; DNA; 9 BP.
XX
AC ABQ72126;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2424.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 62; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 0 A; 3 C; 4 G; 2 T; 0 other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 170
AAC73935
ID   AAC73935 standard; cDNA; 10 BP.
XX
AC   AAC73935;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human dendritic cell cDNA base sequence oligonucleotide #22.
XX
KW   Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW   autoimmune disease; tumour; ss.
XX
OS   Homo sapiens.
XX
PN   WO200060074-A1.
XX
PD   12-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-JP02019.
XX
PR   01-APR-1999;   99JP-0095481.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Hashimoto S,  Matsushima K,  Suzuki T;
XX
DR   WPI; 2000-619172/59.
XX
PT   Groups of genes expressed in human dendritic cells at a greater or
PT   lesser extent than in monocytes for investigation and diagnosis of
PT   autoimmune disease and tumors  -
XX
PS   Claim 1; Page 9; 95pp; Japanese.
XX
CC   The present invention describes a group of genes consisting of 100 genes
CC   which are highly expressed in human dendritic cells; a group of genes
CC   which are expressed at a higher frequency in human dendritic cells than
CC   in human monocytes; and a group of genes which are expressed at lower
CC   frequency in human dendritic cells than in human monocytes. Each group
CC   of genes are characterised in that cDNAs of these genes respectively
CC   have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
CC   SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
CC   (AAC74114 to AAC74213), each is continuous with the base sequence
CC   5'-CATG-3' located most closely to the poly-A region. The sequences can
CC   be used for the investigation of the role and mechanism of the
CC   involvement of dendritic cells in the immune system and for the study and
CC   diagnosis of diseases in which dendritic cells play a significant role,
CC   e.g. cancers and autoimmune diseases.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 171
ABA06204
ID   ABA06204 standard; cDNA; 10 BP.
XX
AC   ABA06204;
XX
DT   10-JAN-2002  (first entry)
XX
DE   Human normal hepatocyte expression gene cDNA, SEQ ID NO: 181.
XX
KW   Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001211883-A.
XX
PD   07-AUG-2001.
XX
PF   31-JAN-2000; 2000JP-0023170.
XX
PR   31-JAN-2000; 2000JP-0023170.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-629566/73.
XX
PT   Human normal hepatocyte expression gene group  -
XX
PS   Claim 1; Page 9; 26pp; Japanese.
XX
CC   The invention relates to a human normal hepatocyte expression gene
CC   group comprising 200 genes in the human normal hepatocyte. The
CC   cDNA of each gene comprises one of 200 fully defined nucleotide
CC   sequences as given in the specification. The gene group and the cDNAs
CC   corresponding to each of the genes in the group are useful in the
CC   diagnosis and treatment of human hepatopathy. The present sequence
CC   is a cDNA corresponding to a gene expressed by normal human
CC   hepatocytes.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 172
AAH64388
ID   AAH64388 standard; cDNA; 10 BP.
XX
AC   AAH64388;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1228.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
```

```
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 173
AAH64389
ID   AAH64389 standard; cDNA; 10 BP.
XX
AC   AAH64389;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1229.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 174
AAH64390
ID   AAH64390 standard; cDNA; 10 BP.
XX
AC   AAH64390;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1230.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 175
AAH64391
ID   AAH64391 standard; cDNA; 10 BP.
XX
AC   AAH64391;
XX
```

```
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1231.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 176
AAH64392
ID   AAH64392 standard; cDNA; 10 BP.
XX
AC   AAH64392;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1232.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 177
AAH64393
ID   AAH64393 standard; cDNA; 10 BP.
XX
AC   AAH64393;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1233.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
```

```
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 178
AAH64394
ID   AAH64394 standard; cDNA; 10 BP.
XX
AC   AAH64394;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1234.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 179
ABV84947
ID   ABV84947 standard; cDNA; 10 BP.
XX
AC   ABV84947;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human multiple HCC highly expressed genes SAGE tag #757.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-0012328.
XX
PR   19-JAN-2001; 2001JP-0012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes -
XX
PS   Claim 64; Page 31; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis
CC   C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC   of the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC   expressed in hepatocellular carcinoma.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 180
ABV78373
ID   ABV78373 standard; cDNA; 10 BP.
XX
AC   ABV78373;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human Th2 cell SAGE tag, SEQ ID NO:84.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th2 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   immune disorder; ss.
XX
```

OS Homo sapiens.
XX
PN JP2002186482-A.
XX
PD 02-JUL-2002.
XX
PF 19-DEC-2000; 2000JP-0385816.
XX
PR 19-DEC-2000; 2000JP-0385816.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-594261/64.
XX
PT Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases -
XX
PS Claim 10; Page 9; 60pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins,
CC and inhibitors of the expression of groups of genes that are expressed
CC in either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78340-ABV78389 are SAGE tags
CC representing 50 genes which are most highly expressed in Th2 cells.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGC 13
||||||||
Db 3 GGCCAGGC 10

RESULT 181
ABL42671
ID ABL42671 standard; cDNA; 10 BP.
XX
AC ABL42671;
XX
DT 12-APR-2002 (first entry)
XX
DE Human maturation/activation dendritic cell expression gene tag #45.
XX
KW Human; maturation/activation dendritic cell expression gene; tag;
KW maturation; activation; dendritic cell; ss.
XX
OS Homo sapiens.
XX
PN JP2001327293-A.
XX
PD 27-NOV-2001.
XX
PF 22-MAY-2000; 2000JP-0150562.
XX
PR 22-MAY-2000; 2000JP-0150562.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-127070/17.
XX
PT Human maturation/activation dendritic cell expression gene group -
XX
PS Claim 1; Page 9; 41pp; Japanese.
XX
CC The present invention describes a human maturation/activation dendritic
CC cell (DC) expression gene group consisting of 100 genes which show the
CC highest expression among the genes expressed in human maturation/
CC activation DC. Also described are: (1) a protein expressed by the above
CC human maturation/activation DC expression gene; (2) an antibody against
CC the protein; and (3) an antagonist against the expression of each gene
CC belonging to the above gene group. The gene group is useful for the
CC treatment and the diagnosis of various human diseases related to human
CC DC. ABL42627 to ABL42926 represent specifically claimed human
CC maturation/activation DC expression gene tags from the present invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGC 13
||||||||
Db 3 GGCCAGGC 10

RESULT 182
AAQ51821/c
ID AAQ51821 standard; RNA; 10 BP.
XX
AC AAQ51821;
XX
DT 25-MAR-2003 (updated)
DT 26-MAY-1994 (first entry)
XX
DE mdr-1 mRNA ribozyme cleavable nucleotide NT585.
XX
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW neuroblastoma; lung cancer; genetic drift; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO9323057-A1.
XX
PD 25-NOV-1993.
XX
PF 13-MAY-1993; 93WO-US04573.
XX
PR 14-MAY-1992; 92US-0882822.
PR 14-MAY-1992; 92US-0882885.
PR 26-AUG-1992; 92US-0936110.
PR 26-AUG-1992; 92US-0936421.
PR 26-AUG-1992; 92US-0936422.
PR 26-AUG-1992; 92US-0936531.
PR 26-AUG-1992; 92US-0936532.
PR 07-DEC-1992; 92US-0987131.
PR 19-JAN-1993; 93US-0006122.
PR 19-JAN-1993; 93US-0008910.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Thompson JD;
XX
DR WPI; 1993-386203/48.
XX
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT associated with tumours or mRNA expressed from gene encoding
PT multiple drug resistance
XX

```
PS   Claim 3; Fig 2; 69pp; English.
XX
CC   The sequences given in AAQ51816-24 represent areas of the multiple
CC   drug resistance (mdr-1) mRNA which are accessible to the ribozyme of
CC   the invention.  The mdr-1 gene encodes a 170 kD integral membrane
CC   protein which confers resistance to certain chemotherapeutic agents,
CC   such as colchicine, doxorubicin, actinomycin D and vinblastine.  The
CC   gene is normally expressed in cells of the colon, small intestine,
CC   kidney, liver and adrenal gland.  High levels of MDR1 transcript
CC   have been found in adenocarcinomas that are intrinsically resistant
CC   to a broad range of chemotherapeutic agents, such as those derived
CC   from adrenal, kidney, liver and bowel.  The ribozymes of the invention
CC   may be used to inhibit the development or expression of a transformed
CC   phenotype in man and other animals by modulating expression of a gene
CC   that contributes to, or inhibits the expression of chronic myelogenous
CC   leukemia (CML), promyelocytic leukemia, follicular lymphoma, B-cell
CC   acute lymphocytic leukemia, breast cancer, colon carcinoma,
CC   neuroblastoma, lung cancer, and other neoplastic conditions.
CC   Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC   cells elicits inhibition of the transformed state.  mdr-1 specific
CC   ribozymes remove the mechanism of drug resistance used by transformed
CC   cells and thus enhances drug therapies for tumours.  The ribozymes may
CC   also be used to study genetic drift and mutations within cells.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 GCCAAAGT 19
               ||||||||
Db          10 GCCAAAGT 3


RESULT 183
AAQ96792
ID   AAQ96792 standard; DNA; 10 BP.
XX
AC   AAQ96792;
XX
DT   26-MAR-1996  (first entry)
XX
DE   HIV-1 NL4-3 nef gene nucleotide deletion 387.
XX
KW   HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO9521912-A1.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-AU00063.
XX
PR   23-DEC-1994;   94AU-0000284.
PR   14-FEB-1994;   94AU-0003864.
PR   21-FEB-1994;   94AU-0004002.
XX
PA   (AURE-) AUSTRALIAN RED CROSS SOC NSW DIV.
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI   Cooper D,  Crowe S,  Deacon NJ,  Learmont JC,  McPhee DA;
XX
DR   WPI; 1995-293115/38.
XX
PT   New non-pathogenic HIV-1 strain carrying a deletion in its nef gene
PT   or LTR region  - can be used in a vaccine to inhibit/reduce
PT   productive infection in an individual by a pathogenic strain
XX
PS   Claim 13; Page 193; 301pp; English.
XX
CC   Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1
CC   or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or
CC   1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the
CC   sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene
CC   (AAQ96141).  The resulting avirulent HIV strains are still capable of
CC   inducing an immune response in humans, and enable the generation of
CC   therapeutic, diagnostic and targeting agents against HIV-1 infection.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 6 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           5 GGGCCAGG 12
               ||||||||
Db           2 GGGCCAGG 9


RESULT 184
AAQ96793
ID   AAQ96793 standard; DNA; 10 BP.
XX
AC   AAQ96793;
XX
DT   26-MAR-1996  (first entry)
XX
DE   HIV-1 NL4-3 nef gene nucleotide deletion 388.
XX
KW   HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO9521912-A1.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-AU00063.
XX
PR   23-DEC-1994;   94AU-0000284.
PR   14-FEB-1994;   94AU-0003864.
PR   21-FEB-1994;   94AU-0004002.
XX
PA   (AURE-) AUSTRALIAN RED CROSS SOC NSW DIV.
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI   Cooper D,  Crowe S,  Deacon NJ,  Learmont JC,  McPhee DA;
XX
DR   WPI; 1995-293115/38.
XX
PT   New non-pathogenic HIV-1 strain carrying a deletion in its nef gene
PT   or LTR region  - can be used in a vaccine to inhibit/reduce
PT   productive infection in an individual by a pathogenic strain
XX
PS   Claim 13; Page 193; 301pp; English.
XX
CC   Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1
CC   or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or
CC   1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the
CC   sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene
CC   (AAQ96141).  The resulting avirulent HIV strains are still capable of
CC   inducing an immune response in humans, and enable the generation of
CC   therapeutic, diagnostic and targeting agents against HIV-1 infection.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           5 GGGCCAGG 12
               ||||||||
Db           1 GGGCCAGG 8
```

```
RESULT 185
AAQ88580/c
ID   AAQ88580 standard; DNA; 10 BP.
XX
AC   AAQ88580;
XX
DT   21-DEC-1995  (first entry)
XX
DE   Human mitochondrial D-loop region DNA probe 6-9.
XX
KW   Tiling strategy; immobilised nucleic acid probe array;
KW   mitochondrial DNA; D-loop region; biological chip;
KW   hybridisation fingerprint; interrogation position; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   10
FT                   /*tag=  a
FT                   /note= "3'-end of probe is covalently attached
FT                          to chip surface"
XX
PN   WO9511995-A1.
XX
PD   04-MAY-1995.
XX
PF   26-OCT-1994;   94WO-US12305.
XX
PR   02-AUG-1994;   94US-0284064.
PR   26-OCT-1993;   93US-0143312.
XX
PA   (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI   Chee M,  Cronin MT,  Fodor SPA,  Gingeras TR,  Huang XC;
PI   Hubbell EA, Lipshutz RJ,  Lobban PE,  Miyada CG,  Morris MS;
PI   Shah N,  Sheldon EL;
XX
DR   WPI; 1995-178887/23.
XX
PT   New arrays of oligo:nucleotide probes - used for comparing known
PT   sequences with variants for detection of mutation(s) and sequencing.
XX
PS   Disclosure; Page 108; 223pp; English.
XX
CC   A DNA chip was prepared for analysing sequences contained in a
CC   1.3kb fragment of human mitochondrial DNA from the D-loop region,
CC   the most polymorphic region of human mitochondrial DNA. The chip
CC   comprised a set of 268 overlapping oligonucleotide probes (see
CC   AAQ88421-Q88684) of varying length (9-14 nucleotides) with varying
CC   overlaps arranged in a 1cm x 1cm array. Each position in the
CC   sequence was represented by at least one probe (usually 2 or more).
CC   DNA was amplified from six human donors and then transcribed to
CC   give the 1.3kb RNA transcripts which were fragmented and hybridised
CC   to the chip. For each individual, a unique hybridisation fingerprint
CC   was produced on the chip; all differences could be correlated with
CC   differences in the cloned genomic DNA sequence.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 5 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCC 9
              ||||||||
Db          8 TCCGGGCC 1


RESULT 186
AAX54584/c
ID   AAX54584 standard; DNA; 10 BP.
XX
AC   AAX54584;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human beta tryptase antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 45; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          8 CCAGGCCA 1


RESULT 187
```

```
AAX18625/c
ID   AAX18625 standard; DNA; 10 BP.
XX
AC   AAX18625;
XX
DT   06-MAY-1999  (first entry)
XX
DE   p53 serial analysis of gene expression tag #9.
XX
KW   p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic;
KW   rat embryo fibroblast; REF; tumour suppressor; cell cycle control;
KW   tumourigenesis; diagnosis; ss.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   WO9901581-A1.
XX
PD   14-JAN-1999.
XX
PF   02-JUL-1998;   98WO-US13903.
XX
PR   02-JUL-1997;   97US-0051573.
XX
PA   (GENZ ) GENZYME CORP.
XX
PI   Beaudry GA,  Bertelsen AH,  Galella EA,  Madden SL;
XX
DR   WPI; 1999-106079/09.
XX
PT   Diagnosis of cancer in potentially neoplastic samples - by comparing
PT   the level of transcription between RNA transcripts in two tissue
PT   samples, useful for providing an extensive profile of gene
PT   expression in rat embryo fibroblast (REF) cells
XX
PS   Example 2; Page 15; 32pp; English.
XX
CC   A method has been developed for the diagnosis of cancer in potentially
CC   neoplastic samples. The method comprises comparing the level of
CC   transcription between RNA transcripts in two tissue samples (which are
CC   of the same type), where the first sample is potentially neoplastic, and
CC   the second sample is normal human tissue. The first sample is
CC   categorized as neoplastic if its level of transcription is lower than
CC   that of the second sample. The transcript is selected from Alu, RAS,
CC   U6 snRNA, 16S RNA, EGR-1, ribosomal protein S27, ETS-1, 28S RNA, CGR11,
CC   and LIMK-2, and it is identified by a tag selected from ribosomal
CC   protein L13a, alpha-tubulin (T1) and (T2), thymosin beta-4, and gamma-
CC   actin. The present sequence represents a serial analysis of gene
CC   expression (SAGE) tag from the present invention. The use of SAGE tags
CC   provides an extensive profile of gene expression in rat embryo
CC   fibroblast (REF) cells containing the (non)-functional p53 tumour
CC   suppression gene. The discovery of new SAGE tags, which are regulated
CC   by p53, enables the diagnosis of genes that are related to cell cycle
CC   control and tumourigenesis.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db          8 GCCAGGCC 1


RESULT 188
AAF20153/c
ID   AAF20153 standard; DNA; 10 BP.
XX
AC   AAF20153;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human beta tryptase polynucleotide fragment #1720.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 141; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          8 CCAGGCCA 15
              ||||||||
Db          8 CCAGGCCA 1


RESULT 189
AAA56555/c
ID   AAA56555 standard; DNA; 10 BP.
XX
AC   AAA56555;
XX
DT   07-SEP-2000  (first entry)
XX
DE   Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:449.
XX
KW   Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW   granulocyte-macrophage colony-stimulating factor; characterisation;
KW   GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW   disease onset mechanism; genetic disease; drug development; ss.
XX
OS   Homo sapiens.
XX
PN   WO200024892-A1.
XX
PD   04-MAY-2000.
XX
PF   28-OCT-1999;   99WO-JP05982.
XX
PR   28-OCT-1998;   98JP-0307532.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Hashimoto S,  Matsushima K,  Suzuki T;
XX
DR   WPI; 2000-350734/30.
XX
PT   Genes most frequently expressed in human monocytes and GM-macrophages
PT   and M-macrophages studied and with cDNAs characterized, for study of
PT   gene specificity, disease onset mechanism, drug development and
PT   diagnosis  -
XX
PS   Claim 43; Page 129; 138pp; Japanese.
XX
CC   The present invention describes 100 human genes, which are expressed
CC   most frequently in human monocytes. The cDNA of each gene has a
CC   sequence fully defined in the specification, and lacking the CATG
CC   sequence located adjacent to polyA region. Also described are:
CC   (1) an antibody specifically for the protein encoded by any of the
CC   genes; (2) oligonucleotides obtained from the cDNA sequences;
CC   (3) 380 human genes which are expressed most frequently in human
CC   macrophages, differentiated from human monocytes by
CC   granulocyte-macrophage colony-stimulating factor, the cDNA of each gene
CC   has a fully defined sequence, given in the specification, lacking the
CC   base sequence CATG located most closely to the poly A region;
CC   (4) an antibody specifically for the protein encoded by any of the
CC   genes of (3); and (5) oligonucleotides obtained from the cDNA sequences
CC   of (3). The genes and cDNAs, are used for the study of gene specificity
CC   and disease onset mechanism e.g. oncogenesis, genetic diseases, drug
CC   development and diagnosis. AAA56107 to AAA56586 represent specifically
CC   claimed oligonucleotide tag sequences for human genes expressed in
CC   monocytes and macrophages.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAA 16
              ||||||||
Db         10 CAGGCCAA 3


RESULT 190
AAA34031/c
ID   AAA34031 standard; DNA; 10 BP.
XX
AC   AAA34031;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:1720.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers  -
XX
PS   Disclosure; Page 478; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          8 CCAGGCCA 15
              ||||||||
Db          8 CCAGGCCA 1


RESULT 191
AAZ77634/c
ID   AAZ77634 standard; DNA; 10 BP.
XX
AC   AAZ77634;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:62.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 65; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAA 16
              ||||||||
Db         10 CAGGCCAA 3


RESULT 192
AAZ79103/c
ID   AAZ79103 standard; DNA; 10 BP.
XX
AC   AAZ79103;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1531.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
```

```
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 109; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
    Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 CCAAAGTC 20
               ||||||||
Db           8 CCAAAGTC 1


RESULT 193
AAZ79322/c
ID   AAZ79322 standard; DNA; 10 BP.
XX
AC   AAZ79322;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1750.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 115; 130pp; English.
XX
```

```
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 194
AAZ81594/c
ID   AAZ81594 standard; DNA; 10 BP.
XX
AC   AAZ81594;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #828.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 80; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAG 11
              ||||||||
Db          8 CGGGCCAG 1


RESULT 195
AAZ82082
ID   AAZ82082 standard; DNA; 10 BP.
XX
AC   AAZ82082;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1316.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
```

```
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 93; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          3 GGGCCAGG 10


RESULT 196
AAZ83064
ID   AAZ83064 standard; DNA; 10 BP.
XX
AC   AAZ83064;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2298.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 121; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          3 GGGCCAGG 10


RESULT 197
AAZ83312/c
ID   AAZ83312 standard; DNA; 10 BP.
XX
AC   AAZ83312;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2546.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
```

```
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 127; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          8 GGGCCAGG 1


RESULT 198
AAZ83787/c
ID   AAZ83787 standard; DNA; 10 BP.
XX
AC   AAZ83787;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3021.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 139; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db         10 GGGCCAGG 3


RESULT 199
AAZ83855
ID   AAZ83855 standard; DNA; 10 BP.
XX
AC   AAZ83855;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3089.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
```

```
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 141; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGC 8
              ||||||||
Db          3 GTCCGGGC 10


RESULT 200
AAZ83864
ID   AAZ83864 standard; DNA; 10 BP.
XX
AC   AAZ83864;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3098.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 141; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 3 A; 5 C; 2 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAA 16
              ||||||||
Db          1 CAGGCCAA 8


RESULT 201
AAZ84284
ID   AAZ84284 standard; DNA; 10 BP.
XX
AC   AAZ84284;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3518.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 152; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          2 GGGCCAGG 9


RESULT 202
AAZ85316/c
ID   AAZ85316 standard; DNA; 10 BP.
XX
AC   AAZ85316;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4550.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 181; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 203
AAZ85453/c
ID   AAZ85453 standard; DNA; 10 BP.
XX
AC   AAZ85453;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4687.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
```

```
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 184; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CCAAAGTC 20
              ||||||||
Db          8 CCAAAGTC 1


RESULT 204
AAZ85585/c
ID   AAZ85585 standard; DNA; 10 BP.
XX
AC   AAZ85585;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4819.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 187; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 2 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          8 GGGCCAGG 1


RESULT 205
AAZ85596/c
ID   AAZ85596 standard; DNA; 10 BP.
XX
AC   AAZ85596;
XX
DT   07-APR-2000  (first entry)
```

```
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4830.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 188; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 6 C; 2 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          8 GGGCCAGG 1


RESULT 206
AAZ85958
ID   AAZ85958 standard; DNA; 10 BP.
XX
AC   AAZ85958;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5192.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 196; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 6 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          2 GGGCCAGG 9


RESULT 207
ABA06090
ID   ABA06090 standard; cDNA; 10 BP.
```

XX
AC ABA06090;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 67.
XX
KW Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS Homo sapiens.
XX
PN JP2001211883-A.
XX
PD 07-AUG-2001.
XX
PF 31-JAN-2000; 2000JP-0023170.
XX
PR 31-JAN-2000; 2000JP-0023170.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-629566/73.
XX
PT Human normal hepatocyte expression gene group -
XX
PS Claim 1; Page 7; 26pp; Japanese.
XX
CC The invention relates to a human normal hepatocyte expression gene
CC group comprising 200 genes in the human normal hepatocyte. The
CC cDNA of each gene comprises one of 200 fully defined nucleotide
CC sequences as given in the specification. The gene group and the cDNAs
CC corresponding to each of the genes in the group are useful in the
CC diagnosis and treatment of human hepatopathy. The present sequence
CC is a cDNA corresponding to a gene expressed by normal human
CC hepatocytes.
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CAGGCCAA 16
|||||||
Db 2 CAGGCCAA 9

RESULT 208
AAH63781
ID AAH63781 standard; cDNA; 10 BP.
XX
AC AAH63781;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 621.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
PS Claim 13; Page 53; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCCAGG 12
|||||||
Db 1 GGGCCAGG 8

RESULT 209
AAH64036/c
ID AAH64036 standard; cDNA; 10 BP.
XX
AC AAH64036;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 876.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
PS Claim 13; Page 59; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX

```
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 210
AAH64037/c
ID   AAH64037 standard; cDNA; 10 BP.
XX
AC   AAH64037;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 877.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 59; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 211
AAH64374/c
ID   AAH64374 standard; cDNA; 10 BP.
XX
AC   AAH64374;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1214.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 212
AAH64375/c
ID   AAH64375 standard; cDNA; 10 BP.
XX
AC   AAH64375;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1215.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
```

```
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 213
AAH32825
ID   AAH32825 standard; cDNA; 10 BP.
XX
AC   AAH32825;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:198.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001069993-A.
XX
PD   21-MAR-2001.
XX
PF   28-APR-2000; 2000JP-0131079.
XX
PR   08-JUL-1999;   99JP-0195103.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-304369/32.
XX
PT   LPS activated human monocyte expression gene group  -
XX
PS   Claim 19; Page 36; 52pp; Japanese.
XX
CC   The present invention describes an lipopolysaccharide (LPS) activated
CC   human monocyte expression gene group consisting of the high-ranking 50
CC   genes of the highest expression among the genes expressed by human
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC   development of new means for the diagnosis and the treatment of various
CC   human diseases in which human monocyte plays an important role.
CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC   monocyte expression gene cDNA tags from the present invention. AAH32944
CC   represents an LPS activated human monocyte expression gene cDNA sequence
CC   encoding AAB98009, which are given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          1 GGGCCAGG 8


RESULT 214
AAH32856/c
ID   AAH32856 standard; cDNA; 10 BP.
XX
AC   AAH32856;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:229.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001069993-A.
XX
PD   21-MAR-2001.
XX
PF   28-APR-2000; 2000JP-0131079.
XX
PR   08-JUL-1999;   99JP-0195103.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-304369/32.
XX
PT   LPS activated human monocyte expression gene group  -
XX
PS   Claim 19; Page 39; 52pp; Japanese.
XX
CC   The present invention describes an lipopolysaccharide (LPS) activated
CC   human monocyte expression gene group consisting of the high-ranking 50
CC   genes of the highest expression among the genes expressed by human
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC   development of new means for the diagnosis and the treatment of various
CC   human diseases in which human monocyte plays an important role.
CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC   monocyte expression gene cDNA tags from the present invention. AAH32944
CC   represents an LPS activated human monocyte expression gene cDNA sequence
CC   encoding AAB98009, which are given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 215
AAF39487/c
ID   AAF39487 standard; DNA; 10 BP.
XX
```

```
AC   AAF39487;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6226.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis
PT   of gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle -
XX
PS   Example; Page 222; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
CC   progression comprising contacting human DNA with a probe which comprises
CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC   member of a class of drugs having a characteristic effect on gene
CC   expression in a yeast cell comprising contacting a yeast cell with a
CC   candidate drug and monitoring expression in the yeast cell of at least 1
CC   NORF gene whose expression is affected by the class of drugs. The NORF
CC   genes may be used to study, monitor and affect phases of the cell cycle,
CC   the differentially expressed genes may be used as markers of phases of
CC   the cell cycle. The methods may be used to identify candidate drugs which
CC   affect the cell cycle and for identification of antifungal drugs.
CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC   primers used in the SAGE method, in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAGT 19
                ||||||||
Db          8 GCCAAAGT 1
```

```
RESULT 216
AAF41493/c
ID   AAF41493 standard; DNA; 10 BP.
XX
AC   AAF41493;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8232.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis
PT   of gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle -
XX
PS   Example; Page 294; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a
CC   yeast cell; and (b) monitoring expression of a NORF gene whose
CC   expression varies as in M1, where a test substance which modifies the
CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
CC   (M3) for identifying human genes which are involved in cell cycle
CC   progression comprising contacting human DNA with a probe which comprises
CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC   member of a class of drugs having a characteristic effect on gene
CC   expression in a yeast cell comprising contacting a yeast cell with a
CC   candidate drug and monitoring expression in the yeast cell of at least 1
CC   NORF gene whose expression is affected by the class of drugs. The NORF
CC   genes may be used to study, monitor and affect phases of the cell cycle,
CC   the differentially expressed genes may be used as markers of phases of
CC   the cell cycle. The methods may be used to identify candidate drugs which
CC   affect the cell cycle and for identification of antifungal drugs.
CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC   primers used in the SAGE method, in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
```

```
              ||||||||
Db          9 CCAGGCCA 2


RESULT 217
ABV84307
ID   ABV84307 standard; cDNA; 10 BP.
XX
AC   ABV84307;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human chronic hepatitis C tissue underexpressed EST SAGE tag #117.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; EST; expressed sequence tag;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-0012328.
XX
PR   19-JAN-2001; 2001JP-0012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes -
XX
PS   Claim 10; Page 13; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis
CC   C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC   of the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84291-ABV84390 are SAGE tags representing the 100 least highly
CC   expressed genes out of those genes which are underexpressed in chronic
CC   hepatitis C liver tissue compared with normal liver tissue.
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAA 17
              ||||||||
Db          2 AGGCCAAA 9


RESULT 218
ABV84789
ID   ABV84789 standard; cDNA; 10 BP.
XX
AC   ABV84789;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human gamma-glutamyltransferase 1 SAGE tag #599.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-0012328.
XX
PR   19-JAN-2001; 2001JP-0012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes -
XX
PS   Claim 46; Page 27; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis
CC   C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC   of the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84691-ABV84790 are SAGE tags representing the 100 least highly
CC   expressed genes out of those genes which are underexpressed in
CC   hepatocellular carcinoma compared with chronic hepatitis C liver tissue.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          3 GGGCCAGG 10


RESULT 219
ABV78459
ID   ABV78459 standard; cDNA; 10 BP.
XX
AC   ABV78459;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:170.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th1 cell;
```

KW activated T cell; T lymphocyte; immune response; expression pattern;
KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.
XX
OS Homo sapiens.
XX
PN JP2002186482-A.
XX
PD 02-JUL-2002.
XX
PF 19-DEC-2000; 2000JP-0385816.
XX
PR 19-DEC-2000; 2000JP-0385816.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-594261/64.
XX
PT Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases -
XX
PS Claim 19; Page 11; 60pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins,
CC and inhibitors of the expression of groups of genes that are expressed
CC in either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC representing 171 genes which are more highly expressed in Th1 cells
CC compared with Th2 cells.
XX
SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGCCAAAG 18
||||||||
Db 1 GGCCAAAG 8

RESULT 220
ABL57664
ID ABL57664 standard; DNA; 10 BP.
XX
AC ABL57664;
XX
DT 08-OCT-2002 (first entry)
XX
DE Human SCYA24 primer-extension oligonucleotide #19.
XX
KW SCYA24; human; small inducible cytokine; isogene; antiasthmatic; asthma;
KW gene therapy; respiratory inflammatory disease; polymorphism; primer;
KW primer extension; ss.
XX
OS Homo sapiens.
XX
PN WO200220851-A1.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28328.
XX
PR 08-SEP-2000; 2000US-231129P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Han J, Kazemi A;
XX
DR WPI; 2002-351785/38.
XX
PT New genetic variants of small inducible cytokine subfamily A member 24
PT gene, useful in studying expression and function of the protein, and
PT for screening drugs to treat diseases such as asthma -
XX
PS Claim 18; Page 15; 98pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising a
CC small inducible cytokine subfamily A (cys-cys), member 24 (SCYA24)
CC isogene. The polypeptide of the invention has antiasthmatic activity. The
CC polynucleotide may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful in the the development of drugs for treating
CC diseases associated with SCYA24 activity, e.g. respiratory inflammatory
CC diseases such as asthma. The 3' end sequences of oligonucleotide primers
CC used for detecting polymorphisms in the SCYA24 gene by primer extension
CC are represented in ABL57646-ABL57675.
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCCAGG 12
||||||||
Db 3 GGGCCAGG 10

RESULT 221
ABK95840
ID ABK95840 standard; DNA; 10 BP.
XX
AC ABK95840;
XX
DT 24-SEP-2002 (first entry)
XX
DE Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #11.
XX
KW Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KW glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KW amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO200244198-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US44781.
XX
PR 30-NOV-2000; 2000US-250254P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Kazemi A, Russo DP, Sausker EA;
XX
DR WPI; 2002-519580/55.
XX
PT Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency
PT and reliability in drug development for treating cancers -
XX
PS Claim 17; Page 16; 139pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC first nucleotide sequence which comprises solute carrier family 1
CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes

CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
CC which is a polymorphic variant of a reference sequence for SLC1A4
CC protein. Also described are methods for: (1) haplotyping or genotyping
CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
CC gene of an individual; (3) identifying an association between a trait and
CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful
CC in screening for drugs targeting (III) that are useful for treating
CC cancer, neurological diseases and amino acid transporter disorders. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with SLC1A4 activity. The haplotyping method is also
CC used by the pharmaceutical research scientist to validate SLC1A4 as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
CC and amino acid transporter disorders, and in the design of clinical
CC trials for treating a specific condition of disease associated with
CC SLC1A4 activity. The methods are also useful for screening compounds
CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
CC prognostic and therapeutic methods. ABK95761-ABK95877 represent
CC SLC1A4 gene allele-specific oligonucleotides, primer extension
CC oligonucleotides and related PCR primers used to identify single
CC nucleotide polymorphisms (SNP) of the gene.
XX
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCCAGGCC 14
||||||||
Db 2 GCCAGGCC 9

RESULT 222
ABK72637/c
ID ABK72637 standard; DNA; 10 BP.
XX
AC ABK72637;
XX
DT 30-JUL-2002 (first entry)
XX
DE Leukotriene B4 receptor primer extension oligonucleotide #9.
XX
KW Human; leukotriene B4; receptor; chemokine receptor-like 1; LTB4R;
KW chemoattractant; inflammation; immune response; infection;
KW inflammatory disorder; recombinant non-human animal;
KW primer extension oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200230949-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US32002.
XX
PR 13-OCT-2000; 2000US-240223P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Chew A, Koshy B, Sanchis A, Sausker EA;
XX
DR WPI; 2002-416857/44.
XX
PT Novel isolated human leukotriene B4 receptor polynucleotide, useful for
PT therapeutic purposes, for studying expression and function of the
PT polynucleotide, and for expressing the receptor -
XX
PS Claim 17; Page 14; 69pp; English.
XX
CC The invention describes an isolated human leukotriene B4 receptor
CC (chemokine receptor-like 1) (LTB4R) polynucleotide (I) comprising a
CC sequence which is a polymorphic variant for a reference sequence for the
CC LTB4R gene or its fragment, or a polymorphic variant of a reference
CC sequence for a LTB4R cDNA or its fragment. LTB4R is a potent
CC chemoattractant that is primarily involved in inflammation, immune
CC responses and host defense against infection. (I) is useful in studying
CC the expression and function of LTB4R, and in expressing LTB4R protein for
CC use in screening for candidate drugs to treat diseases related to LTB4R
CC activity, e.g. inflammatory disorders. A recombinant non-human animal is
CC useful for studying expression of the LTB4R isogenes in vivo, for in vivo
CC screening and testing of drugs targeted against LTB4R protein, and for
CC testing the efficacy of therapeutic agents and compounds for diseases
CC associated with LTB4R activity, e.g. inflammatory disorders, in a
CC biological system. This sequence represents a primer extension
CC oligonucleotide used for detecting polymorphisms in the leukotriene
CC B4 receptor (LTB4R) gene.
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCGGGCCA 10
||||||||
Db 10 CCGGGCCA 3

RESULT 223
ABK17015/c
ID ABK17015 standard; DNA; 10 BP.
XX
AC ABK17015;
XX
DT 26-MAR-2002 (first entry)
XX
DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) primer #38.
XX
KW Pyridoxal kinase; pyridoxine; vitamin B6; PDXK
KW autoimmune polyglandular disease type 1; transgenic animal;
KW gene therapy; primer extension; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190125-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16909.
XX
PR 24-MAY-2000; 2000US-206664P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Duda A, Koshy B;
XX
DR WPI; 2002-106169/14.
XX
PT Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNts,
PT useful for therapeutic purposes, for studying the expression and
PT function of the polyNt, and for expressing pyridoxal protein -
XX
PS Claim 19; Page 14; 135pp; English.
XX
CC The invention describes an isolated human pyridoxal (pyridoxine, vitamin
CC B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in
CC studying the expression and function of PDXK, and in expressing PDXK
CC protein for use in screening for candidate drugs to treat PDXK related
CC diseases and for therapeutic purposes. A transgenic animal is useful for
CC studying expression of the PDXK isogenes in vivo, for in vivo screening
CC and testing of drugs targeted against PDXK protein, and for testing the
CC efficacy of therapeutic agents and compounds for autoimmune polyglandular
CC disease type 1. The polypeptide is useful for studying the effect of the
CC variation on the biological activity of PDXK and the binding affinity of

```
CC   candidate drugs targeting PDXK for the treatment of autoimmune
CC   polyglandular disease type 1. Genotyping and haplotyping is useful for
CC   improving the efficacy and reliability of several steps in the discovery
CC   and development of drugs for treating diseases associated with PDXK
CC   activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK
CC   as a candidate agent for treating a specific condition or disease
CC   predicted to be associated with PDXK activity, and in the design of
CC   clinical trials of candidate drugs. This sequence is one of 38 (see
CC   ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms
CC   by primer extension terminates, described in the method of the invention.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 224
AAS99416
ID   AAS99416 standard; DNA; 10 BP.
XX
AC   AAS99416;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Aldehyde dehydrogenase 5 family, member A1, oligonucleotide #109.
XX
KW   Aldehyde dehydrogenase 5 family member A1; ALDH5A1;
KW   succinate-semialdehyde dehydrogenase; gene therapy; primer;
KW   antisense technology; primer extension oligonucleotide;
KW   4-hydroxybutyric aciduria; metabolic disease; transgenic animal;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200190119-A2.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-US16558.
XX
PR   19-MAY-2000; 2000US-205849P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kliem SE,  Koshy B,  Tanguay DA;
XX
DR   WPI; 2002-089912/12.
XX
PT   New genetic variants of human aldehyde dehydrogenase 5 family, member
PT   A1, ALDH5A1 gene for treating metabolic diseases and for expressing
PT   ALDH5A1 protein useful in identifying drugs to treat 4-hydroxybutyric
PT   aciduria  -
XX
PS   Claim 18; Page 15; 151pp; English.
XX
CC   The invention describes an isolated polynucleotide comprising a
CC   nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for the aldehyde dehydrogenase 5 family, member A1
CC   (succinate-semialdehyde dehydrogenase) (ALDH5A1) gene or its fragment.
CC   The polypeptide is useful for screening for drugs targeting it by
CC   contacting the ALDH5A1 polymorphic variant with a candidate agent and
CC   assaying for binding activity. The polypeptide and haplotypes are useful
CC   for identifying an association between a trait such as a clinical
CC   response to a drug targeting ALDH5A1 and a haplotype ALDH5A1 gene.
CC   Transgenic animals are also useful for studying expression of the ALDH5A1
CC   isogenes in vivo, for in vivo screening and testing of drugs against
CC   ALDH5A1 protein and for testing the efficacy of therapeutic agents and
CC   compounds for 4-hydroxybutyric aciduria and metabolic diseases in a
CC   biological system. Antibodies are useful for diagnostic and prognostic
CC   formats and therapeutic methods, for immunoprecipitating the polypeptide
CC   from solution, for detecting ALDH5A1 protein isoforms in biological
CC   samples, frozen tissue sections, for use in immunocytochemical,
CC   immunohistochemical and immunofluorescence techniques. The polynucleotide
CC   is useful for gene therapy and antisense gene therapy. This sequence is
CC   a primer extension oligonucleotide used to detect polymorphisms in the
CC   ALDH5A1 gene described in the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 6 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          2 GGGCCAGG 9


RESULT 225
AAS95685
ID   AAS95685 standard; DNA; 10 BP.
XX
AC   AAS95685;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Superoxide dismutase 1 (SOD1) allele-specific oligonucleotide #26.
XX
KW   Superoxide dismutase 1; soluble amyotrophic lateral sclerosis 1 (adult);
KW   haplotyping; SOD1; allele-specific oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
PN   WO200185741-A2.
XX
PD   15-NOV-2001.
XX
PF   07-MAY-2001; 2001WO-US14772.
XX
PR   05-MAY-2000; 2000US-202491P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Bentivegna SC,  Kliem SE,  Koshy B,  Parks KE;
XX
DR   WPI; 2002-055578/07.
XX
PT   Isolated human superoxide dismutase 1 (SOD1) soluble polynucleotide,
PT   useful for screening therapeutic compounds, comprises a sequence which
PT   is a polymorphic variant of reference sequence for the SOD1 gene or its
PT   fragment -
XX
PS   Claim 17; Page 13; 70pp; English.
XX
CC   The invention relates to an isolated human superoxide dismutase 1,
CC   soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1) polynucleotide
CC   (I) comprising a sequence which is a polymorphic variant of a reference
CC   sequence for the SOD1 gene. Haplotyping the SOD1 gene of an individual,
CC   involves: (a) determining whether the individual has one of the SOD1
CC   haplotypes or haplotype pairs given in the specification; or
CC   (b) determining for one copy of the SOD1 gene present in the individual,
CC   the identity of the nucleotide at two or more polymorphic sites selected
CC   from PS1-7. The method is useful for determining whether an individual
CC   has a haplotype or haplotype pairs defined in the specification. The
CC   method is also useful for improving the efficacy and reliability of
CC   several steps in the discovery and development of drugs for treating
CC   diseases associated with SOD1 activity, e.g., amyotrophic lateral
CC   sclerosis, and to validate SOD1 as a candidate agent for treating a
CC   specific condition or disease associated with SOD1 activity. It can
CC   further be used in the design of clinical trials of candidate drugs for
```

```
CC   treating a specific condition or disease predicted to be associated with
CC   SOD1 activity. (I) is useful in studying the expression and function of
CC   SOD1, and in expressing SOD1 protein for use in screening for candidate
CC   drugs to treat diseases related to SOD1 activity. AAS95660-AAS95710
CC   represent human superoxide dismutase 1, soluble (amyotrophic lateral
CC   sclerosis 1 (adult)) (SOD1) allele-specific oligonucleotides and
CC   related PCR primers as described in the method of the invention.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db          1 GCCAGGCC 8


RESULT 226
ABL36370
ID   ABL36370 standard; DNA; 10 BP.
XX
AC   ABL36370;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human lysosomal acid phosphatase 2 primer-extension oligonucleotide 6.
XX
KW   Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;
KW   lysosome-specific enzyme; orthophosphoric monoester hydrolysis;
KW   Hodgkin's disease; HD; acid phosphatase deficiency;
KW   novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;
KW   transgenic animal; primer; probe; primer-extension oligonucleotide;
KW   SNP; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200194362-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US18457.
XX
PR   07-JUN-2000; 2000US-210047P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kliem SE,  Messer C,  Tanguay DA;
XX
DR   WPI; 2002-154563/20.
XX
PT   Novel genetic variants of acid phosphatase 2, lysosomal polypeptide
PT   gene useful in studying expression and function of the protein, and for
PT   screening drugs to treat diseases e.g. Hodgkin's disease  -
XX
PS   Claim 19; Page 15; 109pp; English.
XX
CC   The invention comprises the human lysosomal acid phosphatase 2 (ACP2)
CC   nucleic acid and protein sequences. Specifically, the invention relates
CC   to the discovery of 22 novel polymorphic sites within the APC2 gene. The
CC   invention also comprises methods for haplotyping and genotyping the ACP2
CC   gene in an individual. The ACP2 gene (located on chromosome 11) encodes a
CC   lysosomal-specific enzyme that catalyses the hydrolysis of
CC   orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and
CC   protein are pharmaceutically important in the treatment of Hodgkin's
CC   disease (HD) and acid phosphatase deficiency. The novel ACP2 gene
CC   polymorphisms of the invention are useful in haplotyping the ACP2 gene.
CC   ACP2 haplotyping is useful in validating ACP2 as a target (and designing
CC   drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's
CC   disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are
CC   useful for ACP2 genotyping, which can also be used to develop diagnostic
CC   tests and therapeutic treatments. The ACP2 protein and nucleic acids of
CC   the invention are useful in the production of a transgenic animal which
CC   expresses ACP2 protein. The ACP2 nucleic acids of the invention are
CC   useful in the production of allele-specific oligonucleotides designed to
CC   genotype each of the ACP2 polymorphisms. Nucleic acids ABL36299-ABL36320
CC   represent claimed ACP2 allele-specific probes. Nucleic acids ABL36321-
CC   ABL36364 represent claimed ACP2 allele-specific PCR primers. Nucleic
CC   acids ABL36365-ABL36408 represent claimed ACP2 primer-extension
CC   oligonucleotides.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCC 9
              ||||||||
Db          3 TCCGGGCC 10


RESULT 227
ABL42760
ID   ABL42760 standard; cDNA; 10 BP.
XX
AC   ABL42760;
XX
DT   12-APR-2002  (first entry)
XX
DE   Human maturation/activation dendritic cell expression gene tag #134.
XX
KW   Human; maturation/activation dendritic cell expression gene; tag;
KW   maturation; activation; dendritic cell; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001327293-A.
XX
PD   27-NOV-2001.
XX
PF   22-MAY-2000; 2000JP-0150562.
XX
PR   22-MAY-2000; 2000JP-0150562.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-127070/17.
XX
PT   Human maturation/activation dendritic cell expression gene group -
XX
PS   Claim 10; Page 12; 41pp; Japanese.
XX
CC   The present invention describes a human maturation/activation dendritic
CC   cell (DC) expression gene group consisting of 100 genes which show the
CC   highest expression among the genes expressed in human maturation/
CC   activation DC. Also described are: (1) a protein expressed by the above
CC   human maturation/activation DC expression gene; (2) an antibody against
CC   the protein; and (3) an antagonist against the expression of each gene
CC   belonging to the above gene group. The gene group is useful for the
CC   treatment and the diagnosis of various human diseases related to human
CC   DC. ABL42627 to ABL42926 represent specifically claimed human
CC   maturation/activation DC expression gene tags from the present invention.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAA 16
              ||||||||
Db          2 CAGGCCAA 9
```

```
RESULT 228
ABL42855/c
ID   ABL42855 standard; cDNA; 10 BP.
XX
AC   ABL42855;
XX
DT   12-APR-2002  (first entry)
XX
DE   Human maturation/activation dendritic cell expression gene tag #229.
XX
KW   Human; maturation/activation dendritic cell expression gene; tag;
KW   maturation; activation; dendritic cell; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001327293-A.
XX
PD   27-NOV-2001.
XX
PF   22-MAY-2000; 2000JP-0150562.
XX
PR   22-MAY-2000; 2000JP-0150562.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-127070/17.
XX
PT   Human maturation/activation dendritic cell expression gene group -
XX
PS   Claim 19; Page 15; 41pp; Japanese.
XX
CC   The present invention describes a human maturation/activation dendritic
CC   cell (DC) expression gene group consisting of 100 genes which show the
CC   highest expression among the genes expressed in human maturation/
CC   activation DC. Also described are: (1) a protein expressed by the above
CC   human maturation/activation DC expression gene; (2) an antibody against
CC   the protein; and (3) an antagonist against the expression of each gene
CC   belonging to the above gene group. The gene group is useful for the
CC   treatment and the diagnosis of various human diseases related to human
CC   DC. ABL42627 to ABL42926 represent specifically claimed human
CC   maturation/activation DC expression gene tags from the present invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAG 11
              ||||||||
Db          8 CGGGCCAG 1


RESULT 229
ABQ81865
ID   ABQ81865 standard; DNA; 11 BP.
XX
AC   ABQ81865;
XX
DT   19-NOV-2002  (first entry)
XX
DE   Kaposi's Sarcoma SAGE library Tag No.15 SEQ ID NO:15.
XX
KW   Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss.
XX
OS   Homo sapiens.
XX
PN   EP1225233-A2.
XX
PD   24-JUL-2002.
XX
PF   23-JAN-2002; 2002EP-0075264.
XX
PR   23-JAN-2001; 2001EP-0200228.
PR   28-SEP-2001; 2001EP-0203703.
PR   28-SEP-2001; 2001US-325722P.
XX
PA   (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
PI   Van Der Kuyl AC,  Cornelissen M;
XX
DR   WPI; 2002-668396/72.
XX
PT   Determining presence of a tumor cell or angiogenesis, and the
PT   effectiveness of treatment, by detecting the presence of marker genes
PT   is useful to detect and monitor treatment of Kaposi's Sarcoma  -
XX
PS   Claim 12; Page 8; 38pp; English.
XX
CC   The present invention describes a method for determining if an individual
CC   has a tumour cell or site of angiogenesis, or if a treatment is effective
CC   in changing angiogenesis or changing a status of a set of target cells,
CC   comprising determining if a sample of the subject has an expression
CC   product of at least one marker gene. Also described is a compound capable
CC   of altering the expression or activity of Keratin 14, TIE 1, Salioadhesin
CC   or Siglec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed
CC   Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from
CC   the present invention can be used in a diagnostic method, particularly as
CC   an indicator of angiogenesis or to determine presence of a tumour cell.
CC   The method of the invention is suitable to determine within a few days if
CC   a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to
CC   ABQ82006 represent nucleotide sequence used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCC 14
              | ||||  ||||
Db          1 CAGGCCTGGCC 11


RESULT 230
ABV64637
ID   ABV64637 standard; cDNA; 11 BP.
XX
AC   ABV64637;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2423.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
```

PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 92; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGGGCCAGGCC 14
| |||| ||||
Db 1 CAGGCCTGGCC 11

RESULT 231
ABV69138
ID ABV69138 standard; cDNA; 11 BP.
XX
AC ABV69138;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6924.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 217; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGGGCCAGGC 13
| ||||| |||
Db 1 CTGGGCCTGGC 11

RESULT 232
ABQ86573
ID ABQ86573 standard; cDNA; 11 BP.
XX
AC ABQ86573;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 328.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15178.
XX
PR 03-JAN-2001; 2001DE-1000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and ageing, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential
PT gene expression -
XX
PS Claim 8; Page 50; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGGGCCAGGC 13
| ||||| |||
Db 1 CTGGGCCTGGC 11

```
RESULT 233
ABZ72939/c
ID   ABZ72939 standard; RNA; 12 BP.
XX
AC   ABZ72939;
XX
DT   09-APR-2003  (first entry)
XX
DE   Rod opsin hammerhead ribozyme oligonucleotide.
XX
KW   Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease;
KW   target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW   diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW   blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200288320-A2.
XX
PD   07-NOV-2002.
XX
PF   01-MAY-2002; 2002WO-US13679.
XX
PR   01-MAY-2001; 2001US-0847601.
XX
PA   (UYFL ) UNIV FLORIDA.
XX
PI   Lewin AS,  Shaw LC,  Grant MB;
XX
DR   WPI; 2003-111880/10.
XX
PT   A recombinant adeno-associated virus-vectored ribozyme composition,
PT   useful for treating a disease or dysfunction of the mammalian eye e.g.
PT   retinal disease, e.g. diabetic retinopathy or age-related macular
PT   degeneration -
XX
PS   Example 5; Page 73; 115pp; English.
XX
CC   The present invention describes a recombinant adeno-associated virus
CC   (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC   first ribozyme that specifically cleaves an mRNA encoding a protein,
CC   polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC   RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC   alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC   vector comprising a polynucleotide encoding the ribozyme, where the
CC   polynucleotide operably positioned downstream of at least a first
CC   promoter that directs expression of the polynucleotide in a selected
CC   mammalian cell transformed with the vector; (c) a viral particle
CC   comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC   comprising the ribozyme or the polynucleotide; or (e) a host cell
CC   comprising the ribozyme or the polynucleotide. Also described is a method
CC   for decreasing the amount of mRNA encoding a selected polypeptide in a
CC   retinal cell of a mammalian eye, comprising providing to the eye the
CC   composition described above, and for a time effective to specifically
CC   cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC   be used in gene therapy. (I) can be used for treating a disease or
CC   dysfunction of the mammalian eye, such as a retinal disease or retinal
CC   dysfunction, (diabetic) retinopathy, or (age-related) macular
CC   degeneration. (I) is also useful for manufacturing a medicament for
CC   treating the diseases mentioned above, including autosomal dominant
CC   retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC   for treating, decreasing the severity, or ameliorating the symptoms of a
CC   pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC   blindness, a reduction in central or peripheral vision, or a reduction in
CC   total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 12 BP; 3 A; 4 C; 4 G; 1 U; 0 other;

  Query Match           39.0%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity  81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| |||| |
Db         11 GGCCTGGCCTA 1


RESULT 234
AAD03853/c
ID   AAD03853 standard; DNA; 17 BP.
XX
AC   AAD03853;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Human cell cycle checkpoint protein, hchk1 DNA amplifying PCR primer #2.
XX
KW   Human; cell cycle checkpoint; chk1; tumour; malignancy;
KW   cell growth inhibitor; development deficiency; PCR primer;
KW   DNA damage; kinase; ss.
XX
OS   Homo sapiens.
XX
PN   US6218109-B1.
XX
PD   17-APR-2001.
XX
PF   05-SEP-1997;   97US-0924183.
XX
PR   05-SEP-1997;   97US-0924183.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Elledge SJ,  Sanchez Y;
XX
DR   WPI; 2001-289827/30.
XX
PT   New Chk1 proteins and gene sequences encoding the proteins useful as
PT   probes for a portion of the chromosome associated with tumors and other
PT   malignancies, growth and/or development deficiencies  -
XX
PS   Claim 17; Column 24; 37pp; English.
XX
CC   The present sequence is a degenerate PCR primer used for amplifying the
CC   human cell cycle checkpoint protein, hchk1 DNA. The cell cycle
CC   checkpoints are regulatory pathways that control the order and timing of
CC   cell cycle transitions, and ensure that critical events such as DNA
CC   replication and chromosome segregation are completed with high fidelity.
CC   The chk1 protein controls cell cycle in response to DNA damage. It
CC   functions as kinase and phosphorylates the key regulators of Cdk tyrosine
CC   phosphorylation. The checkpoint gene sequences are used as probes for a
CC   portion of the chromosome associated with tumours and other malignancies,
CC   as well as growth and/or development deficiencies. The chk1 proteins are
CC   useful for generating specific antibodies and for inhibiting growth of
CC   cells.
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

  Query Match           39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity  81.8%;  Pred. No. 2.4e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 235
AAS18424/c
ID   AAS18424 standard; DNA; 17 BP.
XX
AC   AAS18424;
XX
DT   12-MAR-2002  (first entry)
```

```
XX
DE   Degenerate PCR primer #2 used to amplify DNA encoding human chk1.
XX
KW   Human; checkpoint protein; hchk1; DNA damage; chromosome 11q24;
KW   cell cycle checkpoint pathway; inhibition of cell growth; tumour;
KW   malignancy; growth deficiency; development deficiency; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6307015-B1.
XX
PD   23-OCT-2001.
XX
PF   12-JAN-2000; 2000US-0488364.
XX
PR   05-SEP-1997;   97US-0924183.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Elledge SJ,  Sanchez Y;
XX
DR   WPI; 2002-040207/05.
XX
PT   New mammalian checkpoint protein and gene, for generating specific
PT   antibodies or for inhibiting the growth of cells, and for use as a
PT   probe for a portion of a chromosome associated with tumours or
PT   malignancies -
XX
PS   Example 1; Column 24; 39pp; English.
XX
CC   The present invention relates to the isolation of human and mouse
CC   checkpoint (chk1) proteins and the nucleic acid sequences encoding them.
CC   Human chk1 (hchk1) maps to chromosome 11q24. Chk1 is involved in
CC   cellular responses to DNA damage, in the cell cycle checkpoint pathway.
CC   The protein is useful for generating specific antibodies and for
CC   inhibiting the growth of cells. The nucleotide sequence encoding the
CC   protein may be used as a probe for a portion of the chromosome
CC   associated with tumours and other malignancies, as well as growth and/or
CC   development deficiencies. The present sequence represents a degenerate
CC   PCR primer used to amplify DNA encoding human chk1 protein.
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 2.4e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 236
ABX16354/c
ID   ABX16354 standard; DNA; 17 BP.
XX
AC   ABX16354;
XX
DT   08-APR-2003  (first entry)
XX
DE   Human checkpoint gene Chk1 PCR primer #2.
XX
KW   Human; checkpoint; chk1; anti-Chk1 antibody; tumour;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002156247-A1.
XX
PD   24-OCT-2002.
XX
PF   12-DEC-2001; 2001US-0020038.
XX
PR   12-JAN-2000; 2000US-0488364.
XX
PA   (ELLE/) ELLEDGE S J.
PA   (SANC/) SANCHEZ Y.
XX
PI   Elledge SJ,  Sanchez Y;
XX
DR   WPI; 2003-182651/18.
XX
PT   New anti-Chk1 antibody, that may be a monoclonal or polyclonal
PT   antibody, useful for detecting a Chk1 protein that is associated with a
PT   tumor -
XX
PS   Example 1; Page 13; 28pp; English.
XX
CC   The invention describes an anti-Chk1 antibody capable of specifically
CC   binding to an antigenic determinant on the proteins encoded by a
CC   sequence comprising 476 (3 sequences), 479, 496 or 513 amino acids.
CC   A new method is used to produce the antibody, which is useful for
CC   detecting a Chk1 protein that is associated with a tumour. This
CC   sequence represents a PCR primer used to isolate DNA encoding the
CC   human checkpoint protein Chk1.
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 2.4e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 237
AAX29342
ID   AAX29342 standard; DNA; 20 BP.
XX
AC   AAX29342;
XX
DT   10-JUN-1999  (first entry)
XX
DE   Chemically modified sense control probe ISIS No: 14318.
XX
KW   Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW   JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KW   hyperproliferative disease; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9909214-A1.
XX
PD   25-FEB-1999.
XX
PF   07-AUG-1998;   98WO-US16488.
XX
PR   13-AUG-1997;   97US-0910629.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Dean N,  Gaarde WA,  Mckay R,  Monia BP,  Nero PS;
XX
DR   WPI; 1999-181060/15.
XX
PT   New antisense oligonucleotides that detect and modulate the
PT   expression of Jun N-terminal kinase proteins  - useful for treating
PT   hyperproliferative diseases and inhibiting tumor growth in animals,
PT   and for modulating protein phosphorylation by these proteins
XX
PS   Example 4; Page 92; 190pp; English.
XX
CC   The invention relates to antisense oligonucleotides that detect and
```

CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal.
XX
SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCC 14
| || |||| || |
Db 7 GGCCTGGCCCGGAC 20

RESULT 238
AAX29331/c
ID AAX29331 standard; DNA; 20 BP.
XX
AC AAX29331;
XX
DT 10-JUN-1999 (first entry)
XX
DE JNK2-specific probe ISIS No: 12560.
XX
KW Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KW hyperproliferative disease; human; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9909214-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-US16488.
XX
PR 13-AUG-1997; 97US-0910629.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean N, Gaarde WA, Mckay R, Monia BP, Nero PS;
XX
DR WPI; 1999-181060/15.
XX
PT New antisense oligonucleotides that detect and modulate the
PT expression of Jun N-terminal kinase proteins - useful for treating
PT hyperproliferative diseases and inhibiting tumor growth in animals,
PT and for modulating protein phosphorylation by these proteins
XX
PS Example 4; Page 87; 190pp; English.
XX
CC The invention relates to antisense oligonucleotides that detect and
CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCC 14
| || |||| || |
Db 14 GGCCTGGCCCGGAC 1

RESULT 239
AAC62874/c
ID AAC62874 standard; DNA; 20 BP.
XX
AC AAC62874;
XX
DT 06-FEB-2001 (first entry)
XX
DE JNK antisense oligonucleotide ISIS #12560.
XX
KW Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
KW cellular hyperproliferation; Alzheimer's; Parkinson's disease;
KW amylotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
KW myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
KW diabetes; Jun N-terminal kinase; ss.
XX
OS Homo sapiens.
XX
PN WO200059549-A1.
XX
PD 12-OCT-2000.
XX
PF 04-APR-2000; 2000WO-US08880.
XX
PR 07-APR-1999; 99US-0287796.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Mckay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
XX
DR WPI; 2000-638427/61.
XX
PT Novel methods for reducing apoptosis comprising contacting cells with
PT antisense oligonucleotides, useful for treating apoptotic disorders,
PT e.g. cancer -
XX
PS Claim 3; Page 133; 160pp; English.
XX
CC The present invention relates to antisense oligonucleotides
CC (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC protein, resulting in decrease of JNK2 expression and leading to
CC induction of apoptosis. The present sequence is one such antisense
CC oligonucleotide. The oligonucleotides of the present invention are useful
CC for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC and cellular hyperproliferation. The oligonucleotides may also be used to
CC increase the stimulation of apoptotic proteins, e.g. for treating
CC Alzheimer's or Parkinson's disease, amylotrophic lateral sclerosis,
CC retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC obstructive jaundice, polycystic kidney and diabetes. The present
CC sequence may have a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCC 14
| || |||| || |
Db 14 GGCCTGGCCCGGAC 1

```
RESULT 240
AAC62885
ID   AAC62885 standard; DNA; 20 BP.
XX
AC   AAC62885;
XX
DT   06-FEB-2001  (first entry)
XX
DE   JNK antisense oligonucleotide ISIS #14318.
XX
KW   Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
KW   cellular hyperproliferation; Alzheimer's; Parkinson's disease;
KW   amylotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
KW   myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
KW   diabetes; Jun N-terminal kinase; ss.
XX
OS   Homo sapiens.
XX
PN   WO200059549-A1.
XX
PD   12-OCT-2000.
XX
PF   04-APR-2000; 2000WO-US08880.
XX
PR   07-APR-1999;   99US-0287796.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Mckay R,  Dean NM,  Monia BP,  Nero PS,  Gaarde WA;
XX
DR   WPI; 2000-638427/61.
XX
PT   Novel methods for reducing apoptosis comprising contacting cells with
PT   antisense oligonucleotides, useful for treating apoptotic disorders,
PT   e.g. cancer -
XX
PS   Example 4; Page 135; 160pp; English.
XX
CC   The present invention relates to antisense oligonucleotides
CC   (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC   specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC   protein, resulting in decrease of JNK2 expression and leading to
CC   induction of apoptosis. The present sequence is one such antisense
CC   oligonucleotide. The oligonucleotides of the present invention are useful
CC   for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC   and cellular hyperproliferation. The oligonucleotides may also be used to
CC   increase the stimulation of apoptotic proteins, e.g. for treating
CC   Alzheimer's or Parkinson's disease, amylotrophic lateral sclerosis,
CC   retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC   obstructive jaundice, polycystic kidney and diabetes. The present
CC   sequence may have a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db          7 GGCCTGGCCCGGAC 20


RESULT 241
AAA48651/c
ID   AAA48651 standard; DNA; 20 BP.
XX
AC   AAA48651;
XX
DT   20-SEP-2000  (first entry)
XX
DE   Antisense oligonucleotide ISIS no.15354 to human JNK2 gene.
XX
KW   Antisense; E-selectin; TNF alpha; cell adhesion;
KW   tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;
KW   sepsis; rheumatoid arthritis; inflammatory; immune disease;
KW   inflammatory bowel disease; allergic contact dermatitis; psoriasis;
KW   diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
KW   immunosuppressive; antipsoriatic; antidiabetic; antithyroid;
KW   cytostatic; dermatological; antiallergic; Ha-ras; c-raf;
KW   c-Jun N-terminal kinase; JNK; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..6
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "All bases are 2'-methoxyethoxy,
FT                   additionally C bases are m5c"
FT   modified_base   7..15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   modified_base   16..20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "All bases are 2'-methoxyethoxy,
FT                   additionally C bases are m5c"
XX
PN   WO200034303-A1.
XX
PD   15-JUN-2000.
XX
PF   08-DEC-1999;   99WO-US28965.
XX
PR   10-DEC-1998;   98US-0209668.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Xu XS;
XX
DR   WPI; 2000-423367/36.
XX
PT   Modulating cell adhesion molecule expression for treating immune or
PT   inflammatory diseases involves treating cell with specific inhibitor of
PT   Tumour Necrosis Factor alpha signalling molecule  -
XX
PS   Claim 36; Page 46; 100pp; English.
XX
CC   A novel method for modulating cell adhesion molecule expression
CC   involves antisense inhibition of a tumour necrosis factor (TNF) alpha
CC   signalling molecule. In the method TNF alpha signalling molecules
CC   Ha-ras, c-raf and c-Jun N-terminal kinase (JNK)2 were inhibited by
CC   antisense oligonucleotides. In addition an antisense oligonucleotide
CC   to the cell adhesion molecule E-selectin was also examined. The
CC   present sequence is the JNK2 antisense oligonucleotide. The
CC   antisense oligonucleotides used in the method contained modifications,
CC   namely phosphorothioate linkages and 2'methoxyethoxy bases. Some C
CC   residues also had a 5'methyl modification. Inhibitors of the TNF alpha
CC   signalling molecules have antibacterial, immunosuppressive,
CC   antipsoriatic, antidiabetic, antithyroid, cytostatic, dermatological,
CC   antiallergic and antiinflammatory activity. The antisense inhibitors
CC   may be useful for the treatment of sepsis, rheumatoid arthritis,
CC   inflammatory, immune disease, inflammatory bowel disease, allergic
CC   contact dermatitis, psoriasis, diabetes, Grave's disease, allograft
CC   rejection and cancer.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 242
AAH23754/c
ID   AAH23754 standard; DNA; 20 BP.
XX
AC   AAH23754;
XX
DT   13-AUG-2001  (first entry)
XX
DE   JNK1 antisense oligonucleotide, JNK2AS, (ISIS #12560).
XX
KW   JNK; jun kinase; antisense; cytostatic; cancer;
KW   2'-O-methoxyethyl oligonucleotide; MOE; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..20
FT                    /*tag=  a
FT                    /mod_base= "OTHER"
FT                    /note= "This oligonucleotide is a 2'-O-methoxyethyl (MOE)
FT                    chimeric antisense oligonucleotide containing five
FT                    MOE/phoshopdiester residues flanking a
FT                    2'-deoxynucleotide/phosphorothioate region"
XX
PN   WO200134792-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US30869.
XX
PR   12-NOV-1999;   99US-0165224.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Potapova O,  Gorospe M,  Holbrook NJ;
XX
DR   WPI; 2001-335925/35.
XX
PT   Use of Jun Kinase antisense mRNA for treating cancer by administering
PT   vector comprising promoter operably linked to DNA sequence that encodes
PT   the antisense mRNA to patient diagnosed with cancer  -
XX
PS   Claim 1; Page 41; 75pp; English.
XX
CC   The present invention relates to the use of Jun Kinase (JNK) antisense
CC   oligonucleotides for treating cancer and for screening compounds that
CC   mimic or augment the effect of JNK antisense oligonucleotides treatment
CC   for cancer. The present sequence is one such JNK antisense
CC   oligonucleotide.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match          38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 243
AAF99183/c
ID   AAF99183 standard; DNA; 20 BP.
XX
AC   AAF99183;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #299.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US26383.
XX
PR   25-SEP-1999;   99US-0156113.
PR   27-SEP-1999;   99US-0156135.
PR   23-AUG-2000; 2000US-0227436.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids -
XX
PS   Claim 101; Page 44; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells.
CC   Note: the present sequence may have a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match          38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 244
ABS77827/c
ID   ABS77827 standard; DNA; 20 BP.
XX
AC   ABS77827;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #311.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis;
KW   psoriasis; diabetic retinopathy; retinopathy of prematurity;
KW   macular degeneration; corneal graft rejection; neovascular glaucoma;
KW   retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;
```

```
KW   myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW   haemophiliac joint; angiofibroma; wound granulation;
KW   intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US48458.
XX
PR   14-DEC-2000; 2000US-255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least
PT   one antiangiogenic nucleic acid molecule to the subject  -
XX
PS   Claim 2; Page 25; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule.
CC   Also included is a kit comprising a first container housing the
CC   antiangiogenic nucleic acids, and instructions for administering them to
CC   a subject having a condition characterised by unwanted angiogenesis.
CC   The method is useful for inhibiting angiogenesis associated with solid
CC   tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC   arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC   macular degeneration, corneal graft rejection, neovascular glaucoma,
CC   retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial
CC   angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
CC   joints, angiofibroma, wound granulation, intestinal adhesions,
CC   atherosclerosis, scleroderma and hypertrophic scars. The present
CC   sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 245
ABL39057/c
ID   ABL39057 standard; DNA; 20 BP.
XX
AC   ABL39057;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 463.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US20154.
XX
PR   22-JUN-2000; 2000US-213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer -
XX
PS   Disclosure; Page 212; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC   non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in
CC   the exemplification of the invention.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 246
AAX54706/c
ID   AAX54706 standard; DNA; 9 BP.
XX
AC   AAX54706;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human fibronectin antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
```

PF 17-SEP-1998; 98WO-US19419.
XX
PR 09-JUN-1998; 98US-0093972.
PR 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
PS Disclosure; Page 55; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAX55272-74. These multiple target
CC oligonucleotides (specifically AAX55180-271) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCCGGGCC 9
|| |||||||
Db 9 GCCCGGGCC 1

RESULT 247
AAF20275/c
ID AAF20275 standard; DNA; 9 BP.
XX
AC AAF20275;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human fibronectin polynucleotide fragment #1842.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 220; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCCGGGCC 9
|| |||||||
Db 9 GCCCGGGCC 1

RESULT 248
AAA34153/c
ID AAA34153 standard; DNA; 9 BP.
XX
AC AAA34153;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1842.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

```
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 495; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 5.2e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCC 9
              | |||||||
Db          9 GCCCGGGCC 1


RESULT 249
ABQ71850
ID   ABQ71850 standard; DNA; 9 BP.
XX
AC   ABQ71850;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2148.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US43438.
XX
PR   20-NOV-2000; 2000US-0716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering,
PT   comprises first, second and third zinc fingers, ordered from N- to
PT   C-terminus -
XX
PS   Example 1; Page 56; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
CC   and specificity for their target sequences, as well as enhanced
CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC   represent DNA target sequences and zinc finger peptides which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 9 BP; 1 A; 2 C; 6 G; 0 U; 0 other;

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 5.2e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 250
ABQ71851
ID   ABQ71851 standard; DNA; 9 BP.
XX
AC   ABQ71851;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2149.
XX
```

```
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US43438.
XX
PR   20-NOV-2000; 2000US-0716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering,
PT   comprises first, second and third zinc fingers, ordered from N- to
PT   C-terminus -
XX
PS   Example 1; Page 56; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
CC   and specificity for their target sequences, as well as enhanced
CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC   represent DNA target sequences and zinc finger peptides which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 9 BP; 1 A; 2 C; 6 G; 0 U; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 5.2e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 251
AAZ82328
ID   AAZ82328 standard; DNA; 10 BP.
XX
AC   AAZ82328;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1562.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 100; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||| ||||
Db          1 GGCCTGGCC 9


RESULT 252
AAZ77977
ID   AAZ77977 standard; DNA; 10 BP.
XX
AC   AAZ77977;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:405.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
```

KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13800.
XX
PR 19-JUN-1998; 98US-0089833.
PR 19-JUN-1998; 98US-0089844.
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089878.
PR 19-JUN-1998; 98US-0089991.
PR 19-JUN-1998; 98US-0089992.
PR 19-JUN-1998; 98US-0089993.
PR 19-JUN-1998; 98US-0089994.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0089999.
PR 19-JUN-1998; 98US-0090000.
PR 19-JUN-1998; 98US-0090035.
PR 19-JUN-1998; 98US-0090036.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PR 19-JUN-1998; 98US-0090042.
PR 19-JUN-1998; 98US-0090043.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090045.
PR 19-JUN-1998; 98US-0090047.
PR 19-JUN-1998; 98US-0090048.
PR 19-JUN-1998; 98US-0090072.
PR 19-JUN-1998; 98US-0090076.
PR 19-JUN-1998; 98US-0090077.
PR 19-JUN-1998; 98US-0090078.
PR 19-JUN-1998; 98US-0090079.
PR 19-JUN-1998; 98US-0090080.
PR 08-DEC-1998; 98US-0111715.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer -
XX
PS Claim 1; Page 76; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or
CC ESTs (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can
CC lyse the tumour cells, immunostimulatory cofactors also being required
CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell
CC differentially expressed genes, or of their encoded proteins, can be used
CC to identify cells as belonging to the monocyte lineage. Cells containing
CC these genes can be used in active immunotherapy (or to stimulate
CC production of a population of antigen-specific effector cells) and
CC vectors containing them are used in gene therapy. Co-administration of
CC tumour antigens and APC-associated costimulatory factors ensures adequate
CC antigen presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells.
XX
SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCCAGGC 13
||||| |||
Db 2 GGGCCTGGC 10

RESULT 253
AAZ84966
ID AAZ84966 standard; DNA; 10 BP.
XX
AC AAZ84966;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4200.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 171; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic

```
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||||| |||
Db          2 GGGCCTGGC 10


RESULT 254
AAH76342
ID   AAH76342 standard; DNA; 10 BP.
XX
AC   AAH76342;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Z. mays Ms45 promoter deletion mutant fragment LS02.
XX
KW   Ms45; male tissue; regulatory region; transcription; male fertility;
KW   hybrid seed; promoter; ss.
XX
OS   Zea mays.
XX
PN   WO200160997-A2.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04527.
XX
PR   15-FEB-2000; 2000US-0504487.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Albertsen MC,  Fox TW,  Garnaat CW,  Huffman G,  Kendall TL;
XX
DR   WPI; 2001-514772/56.
XX
PT   A male tissue-preferred regulatory region comprising nucleotide
PT   sequences essential for initiating transcription of the MS45 gene
PT   useful for mediating fertility in a male plant -
XX
PS   Example 5; Fig 8; 50pp; English.
XX
CC   The invention provides a male tissue-preferred regulatory region (I)
CC   comprising nucleotide sequences essential for initiating transcription
CC   of the MS45 gene. A method of mediating male fertility in a plant is
CC   provided that involves introducing an expression vector comprising a
CC   promoter operably linked to (I) into a plant where the exogenous gene
CC   impacts male fertility of the plant and (I) controls expression of the
CC   exogenous gene. A method of producing hybrid seeds is also provided.
CC   Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC   promoter region, used for determining the essential region of MS45
CC   promoter.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAG 11
              ||||||| |
Db          2 CCGGGCCCG 10


RESULT 255
AAH76345/c
ID   AAH76345 standard; DNA; 10 BP.
XX
AC   AAH76345;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Z. mays Ms45 promoter deletion mutant fragment LS05.
XX
KW   Ms45; male tissue; regulatory region; transcription; male fertility;
KW   hybrid seed; promoter; ss.
XX
OS   Zea mays.
XX
PN   WO200160997-A2.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04527.
XX
PR   15-FEB-2000; 2000US-0504487.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Albertsen MC,  Fox TW,  Garnaat CW,  Huffman G,  Kendall TL;
XX
DR   WPI; 2001-514772/56.
XX
PT   A male tissue-preferred regulatory region comprising nucleotide
PT   sequences essential for initiating transcription of the MS45 gene
PT   useful for mediating fertility in a male plant -
XX
PS   Example 5; Fig 8; 50pp; English.
XX
CC   The invention provides a male tissue-preferred regulatory region (I)
CC   comprising nucleotide sequences essential for initiating transcription
CC   of the MS45 gene. A method of mediating male fertility in a plant is
CC   provided that involves introducing an expression vector comprising a
CC   promoter operably linked to (I) into a plant where the exogenous gene
CC   impacts male fertility of the plant and (I) controls expression of the
CC   exogenous gene. A method of producing hybrid seeds is also provided.
CC   Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC   promoter region, used for determining the essential region of MS45
CC   promoter.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAG 11
              ||||||| |
Db          9 CCGGGCCCG 1


RESULT 256
AAH76348
ID   AAH76348 standard; DNA; 10 BP.
XX
```

```
AC   AAH76348;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Z. mays Ms45 promoter deletion mutant fragment LS08.
XX
KW   Ms45; male tissue; regulatory region; transcription; male fertility;
KW   hybrid seed; promoter; ss.
XX
OS   Zea mays.
XX
PN   WO200160997-A2.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04527.
XX
PR   15-FEB-2000; 2000US-0504487.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Albertsen MC,  Fox TW,  Garnaat CW,  Huffman G,  Kendall TL;
XX
DR   WPI; 2001-514772/56.
XX
PT   A male tissue-preferred regulatory region comprising nucleotide
PT   sequences essential for initiating transcription of the MS45 gene
PT   useful for mediating fertility in a male plant -
XX
PS   Example 5; Fig 8; 50pp; English.
XX
CC   The invention provides a male tissue-preferred regulatory region (I)
CC   comprising nucleotide sequences essential for initiating transcription
CC   of the MS45 gene. A method of mediating male fertility in a plant is
CC   provided that involves introducing an expression vector comprising a
CC   promoter operably linked to (I) into a plant where the exogenous gene
CC   impacts male fertility of the plant and (I) controls expression of the
CC   exogenous gene. A method of producing hybrid seeds is also provided.
CC   Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC   promoter region, used for determining the essential region of MS45
CC   promoter.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCC 9
              | |||||||
Db          1 GGCCGGGCC 9


RESULT 257
AAS19876/c
ID   AAS19876 standard; DNA; 10 BP.
XX
AC   AAS19876;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Oligonucleotide #56 to detect human RANGAP1 gene polymorphisms.
XX
KW   Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KW   chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW   cancer; irregular cell cycle associated disorder; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179240-A2.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-US12455.
XX
PR   17-APR-2000; 2000US-198072P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-075068/10.
XX
PT   Genotyping human Ran GTPase activating protein 1 gene of individual for
PT   determining haplotype of individual, involves determining identity of
PT   nucleotide pair at specific polymorphic sites for two copies of the
PT   gene -
XX
PS   Claim 17; Page 16; 148pp; English.
XX
CC   The present invention relates to novel single nucleotide polymorphisms
CC   (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC   located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC   genotyping the RANGAP1 gene. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC   primer-extension oligonucleotides for detecting the RANGAP1 gene
CC   polymorphisms. The polynucleotides and screened compounds are useful for
CC   treatment of diseases associated with RANGAP1 activity, such as
CC   cancer and other disorders associated with an irregular cell cycle.
CC   AAS19821-AAS19898 represent primer-extension oligonucleotides for
CC   detecting human RANGAP1 gene polymorphisms.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCC 9
              |||| ||||
Db          9 GTCCTGGCC 1


RESULT 258
AAH64374
ID   AAH64374 standard; cDNA; 10 BP.
XX
AC   AAH64374;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1214.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
```

```
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db          1 GCCTGGCCA 9


RESULT 259
AAH64375
ID   AAH64375 standard; cDNA; 10 BP.
XX
AC   AAH64375;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1215.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 67; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db          1 GCCTGGCCA 9


RESULT 260
AAH32856
ID   AAH32856 standard; cDNA; 10 BP.
XX
AC   AAH32856;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:229.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001069993-A.
XX
PD   21-MAR-2001.
XX
PF   28-APR-2000; 2000JP-0131079.
XX
PR   08-JUL-1999;   99JP-0195103.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-304369/32.
XX
PT   LPS activated human monocyte expression gene group  -
XX
PS   Claim 19; Page 39; 52pp; Japanese.
XX
CC   The present invention describes an lipopolysaccharide (LPS) activated
CC   human monocyte expression gene group consisting of the high-ranking 50
CC   genes of the highest expression among the genes expressed by human
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC   development of new means for the diagnosis and the treatment of various
CC   human diseases in which human monocyte plays an important role.
CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC   monocyte expression gene cDNA tags from the present invention. AAH32944
CC   represents an LPS activated human monocyte expression gene cDNA sequence
CC   encoding AAB98009, which are given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db          1 GCCTGGCCA 9


RESULT 261
ABK95840/c
ID   ABK95840 standard; DNA; 10 BP.
XX
AC   ABK95840;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #11.
XX
KW   Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KW   glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KW   amino acid transporter disorder; single nucleotide polymorphism; SNP.
```

```
XX
OS   Homo sapiens.
XX
PN   WO200244198-A2.
XX
PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-US44781.
XX
PR   30-NOV-2000; 2000US-250254P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Kazemi A,  Russo DP,  Sausker EA;
XX
DR   WPI; 2002-519580/55.
XX
PT   Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT   Amino Acid Transporter), Member 4 isogenes, for improving efficiency
PT   and reliability in drug development for treating cancers -
XX
PS   Claim 17; Page 16; 139pp; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising a
CC   first nucleotide sequence which comprises solute carrier family 1
CC   (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
CC   (II) and an isolated polypeptide (III) comprising an amino acid sequence
CC   which is a polymorphic variant of a reference sequence for SLC1A4
CC   protein. Also described are methods for: (1) haplotyping or genotyping
CC   SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
CC   gene of an individual; (3) identifying an association between a trait and
CC   at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful
CC   in screening for drugs targeting (III) that are useful for treating
CC   cancer, neurological diseases and amino acid transporter disorders. The
CC   methods are useful for improving the efficiency and reliability of
CC   several steps in the discovery and development of drugs for treating
CC   diseases associated with SLC1A4 activity. The haplotyping method is also
CC   used by the pharmaceutical research scientist to validate SLC1A4 as a
CC   candidate target for treating a specific condition or disease predicted
CC   to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
CC   and amino acid transporter disorders, and in the design of clinical
CC   trials for treating a specific condition of disease associated with
CC   SLC1A4 activity. The methods are also useful for screening compounds
CC   targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
CC   prognostic and therapeutic methods. ABK95761-ABK95877 represent
CC   SLC1A4 gene allele-specific oligonucleotides, primer extension
CC   oligonucleotides and related PCR primers used to identify single
CC   nucleotide polymorphisms (SNP) of the gene.
XX
SQ   Sequence 10 BP; 1 A; 6 C; 3 G; 0 U; 0 other;

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity  88.9%;  Pred. No. 1.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||||| |||
Db         10 GGGCCTGGC 2


RESULT 262
ABV65097/c
ID   ABV65097 standard; cDNA; 11 BP.
XX
AC   ABV65097;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2883.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 105; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 11;
  Best Local Similarity  88.9%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCA 15
              ||| |||||
Db         10 GCCTGGCCA 2


RESULT 263
ABV69411
ID   ABV69411 standard; cDNA; 11 BP.
XX
AC   ABV69411;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7197.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
```

```
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 226; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 11;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||||| |||
Db          2 GGGCCTGGC 10


RESULT 264
AAA82879
ID   AAA82879 standard; DNA; 19 BP.
XX
AC   AAA82879;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk4 ribozyme binding site #60.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW   restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US28772.
XX
PR   04-DEC-1998;   98US-0110954.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1  -
XX
PS   Disclosure; Page 53; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells.
CC   The ribozyme is resistant to endonuclease activity and hence is
CC   efficient in restenosis treatment.
XX
SQ   Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||| ||||
Db         11 GGCCTGGCC 19


RESULT 265
AAH58041
ID   AAH58041 standard; DNA; 19 BP.
XX
AC   AAH58041;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:465.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US29500.
XX
PR   26-OCT-1999;   99US-0161532.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using
PT   ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT   matrix metalloproteinases, growth factors and cell-cycle dependent
PT   kinases -
XX
PS   Example 1; Page 105; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative
CC   skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
```

```
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||| ||||
Db         11 GGCCTGGCC 19


RESULT 266
AAT09655/c
ID   AAT09655 standard; DNA; 8 BP.
XX
AC   AAT09655;
XX
DT   25-MAR-2003  (updated)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 0 A; 3 C; 2 G; 3 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAA 16
              |||||||
Db          7 AGGCCAA 1


RESULT 267
AAT09656/c
ID   AAT09656 standard; DNA; 8 BP.
XX
AC   AAT09656;
XX
DT   25-MAR-2003  (updated)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 0 A; 2 C; 2 G; 4 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAA 16
              |||||||
Db          7 AGGCCAA 1


RESULT 268
AAT09366
ID   AAT09366 standard; DNA; 8 BP.
XX
AC   AAT09366;
XX
DT   25-MAR-2003  (updated)
```

```
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 4 A; 2 C; 2 G; 0 U; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAA 16
              |||||||
Db          2 AGGCCAA 8


RESULT 269
AAT09389
ID   AAT09389 standard; DNA; 8 BP.
XX
AC   AAT09389;
XX
DT   25-MAR-2003  (updated)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 3 A; 2 C; 3 G; 0 U; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAA 16
              |||||||
Db          1 AGGCCAA 7


RESULT 270
AAT09459
ID   AAT09459 standard; DNA; 8 BP.
XX
AC   AAT09459;
XX
DT   25-MAR-2003  (updated)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
```

```
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 3 A; 2 C; 3 G; 0 U; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAA 16
               |||||||
Db          2 AGGCCAA 8


RESULT 271
AAT09572/c
ID   AAT09572 standard; DNA; 8 BP.
XX
AC   AAT09572;
XX
DT   25-MAR-2003  (updated)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 0 A; 3 C; 2 G; 3 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAA 16
               |||||||
Db          8 AGGCCAA 2


RESULT 272
AAX29560/c
ID   AAX29560 standard; DNA; 8 BP.
XX
AC   AAX29560;
XX
DT   03-JUN-1999  (first entry)
XX
DE   Primer for human G-protein coupled receptor genes.
XX
KW   Nucleic acid amplification; nuclear receptor; G-protein coupled receptor;
KW   apoptosis; DNA repair; DNA replication; plant biology; agriculture;
KW   human; veterinary medicine; reproduction; microbiology; hybridisation;
KW   environmental science; DNA fingerprinting; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9911823-A2.
XX
PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US18392.
XX
PR   05-SEP-1997;   97US-0925816.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   McClelland M,  Pesole G;
XX
DR   WPI; 1999-205200/17.
XX
PT   Subset of primers able to amplify group of related sequences
XX
PS   Claim 21; Page 75; 92pp; English.
XX
CC   The invention provides primers (AAX29501-X29679) for identifying
CC   sequences encoding structurally or functionally related proteins such as
CC   nuclear or G-protein coupled receptors, apoptosis-related or DNA
CC   repair/replication proteins. The identified sequences are broadly useful
CC   in plant biology, agriculture, human or veterinary medicine,
CC   reproduction, microbiology or environmental science, e.g. to study
CC   expression of nuclear receptors at different stages of tissue development
CC   or after treatment with particular drugs. It is also used for DNA
CC   fingerprinting (to generate products useful for differential
CC   hybridisation), or, where a 3'-anchor primer is used, to isolate the
CC   3'-ends of mRNA sequences. Sequences AAX29526-X29583 represent claimed
CC   primers specific for human G-protein coupled receptor genes.
XX
SQ   Sequence 8 BP; 0 A; 4 C; 2 G; 2 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGG 12
               |||||||
Db          8 GGCCAGG 2
```

```
RESULT 273
AAX29558/c
ID   AAX29558 standard; DNA; 8 BP.
XX
AC   AAX29558;
XX
DT   03-JUN-1999  (first entry)
XX
DE   Primer for human G-protein coupled receptor genes.
XX
KW   Nucleic acid amplification; nuclear receptor; G-protein coupled receptor;
KW   apoptosis; DNA repair; DNA replication; plant biology; agriculture;
KW   human; veterinary medicine; reproduction; microbiology; hybridisation;
KW   environmental science; DNA fingerprinting; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9911823-A2.
XX
PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US18392.
XX
PR   05-SEP-1997;   97US-0925816.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   McClelland M,  Pesole G;
XX
DR   WPI; 1999-205200/17.
XX
PT   Subset of primers able to amplify group of related sequences
XX
PS   Claim 21; Page 75; 92pp; English.
XX
CC   The invention provides primers (AAX29501-X29679) for identifying
CC   sequences encoding structurally or functionally related proteins such as
CC   nuclear or G-protein coupled receptors, apoptosis-related or DNA
CC   repair/replication proteins. The identified sequences are broadly useful
CC   in plant biology, agriculture, human or veterinary medicine,
CC   reproduction, microbiology or environmental science, e.g. to study
CC   expression of nuclear receptors at different stages of tissue development
CC   or after treatment with particular drugs. It is also used for DNA
CC   fingerprinting (to generate products useful for differential
CC   hybridisation), or, where a 3'-anchor primer is used, to isolate the
CC   3'-ends of mRNA sequences. Sequences AAX29526-X29583 represent claimed
CC   primers specific for human G-protein coupled receptor genes.
XX
SQ   Sequence 8 BP; 0 A; 4 C; 2 G; 2 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGG 12
              |||||||
Db          7 GGCCAGG 1


RESULT 274
AAA80793
ID   AAA80793 standard; DNA; 8 BP.
XX
AC   AAA80793;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 106.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-0859954.
XX
PR   15-APR-1996;   96US-0632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction
PT   and other primer processes comprises primer walking of octamer
PT   oligonucleotides -
XX
PS   Example 8; Column 77-78; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and
CC   corresponding complementary sequences, where the library primer is
CC   complementary to a known sequence adjacent to the unknown sequence or
CC   is complementary to a sequence in a known extension product. The method
CC   is useful for DNA nucleotide sequencing, in PCR, and in other processes
CC   which make use of primers.  The octamers are used to identify coding
CC   sequences. Primer walking using the octamer libraries is advantageous
CC   over other sequencing methods because it does not require multiple
CC   cloning steps nor subsequent template preparations, and it is a
CC   directed and methodical approach. AAA80688-A81253 represent the octamer
CC   primers used in the primer walking method of the invention.
XX
SQ   Sequence 8 BP; 4 A; 2 C; 2 G; 0 U; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          1 GCCAAAG 7


RESULT 275
AAA81046
ID   AAA81046 standard; DNA; 8 BP.
XX
AC   AAA81046;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 359.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-0859954.
XX
PR   15-APR-1996;   96US-0632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
```

PI Hardin PE, Hardin SH, Homayouni R;
XX
DR WPI; 2000-474852/41.
XX
PT Sequencing an unknown DNA molecule for the polymerase chain reaction
PT and other primer processes comprises primer walking of octamer
PT oligonucleotides -
XX
PS Example 8; Column 205-206; 161pp; English.
XX
CC This invention describes a novel method for sequencing an unknown DNA
CC molecule which comprises selecting a library primer from an octamer
CC oligonucleotide library consisting of 48 8-bp sequences and
CC corresponding complementary sequences, where the library primer is
CC complementary to a known sequence adjacent to the unknown sequence or
CC is complementary to a sequence in a known extension product. The method
CC is useful for DNA nucleotide sequencing, in PCR, and in other processes
CC which make use of primers. The octamers are used to identify coding
CC sequences. Primer walking using the octamer libraries is advantageous
CC over other sequencing methods because it does not require multiple
CC cloning steps nor subsequent template preparations, and it is a
CC directed and methodical approach. AAA80688-A81253 represent the octamer
CC primers used in the primer walking method of the invention.
XX
SQ Sequence 8 BP; 3 A; 3 C; 1 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCAAAGT 19
|||||||
Db 2 CCAAAGT 8

RESULT 276
AAD22387/c
ID AAD22387 standard; DNA; 8 BP.
XX
AC AAD22387;
XX
DT 12-FEB-2002 (first entry)
XX
DE Oligonucleotide #1 to generate fatty acid biosynthesis gene construct.
XX
KW Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;
KW linoleic acid; stearic acid; oleic acid; transgenic plant;
KW cotton seed oil; ss.
XX
OS Unidentified.
XX
PN WO200179499-A1.
XX
PD 25-OCT-2001.
XX
PF 18-APR-2001; 2001WO-AU00436.
XX
PR 18-APR-2000; 2000US-198124P.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Green A, Singh S, Liu Q;
XX
DR WPI; 2001-602932/68.
XX
PT Modifying endogenous oil of cotton plants, to produce cotton seed oil
PT with reduced palmitic and/or linoleic acid content, involves producing
PT transgenic plants containing a fatty acid biosynthesis gene in a
PT construct -
XX
PS Example 11; Page 90; 201pp; English.
XX
CC The invention relates to a method for modifying the endogenous oil of a
CC cotton plant, to produce cotton seed oil. The method comprises producing
CC a transgenic cotton plant having a gene construct which includes a fatty
CC acid biosynthesis gene operably linked to a promoter sequence capable of
CC conferring expression of the delta9-desaturase (delta9 stearoyl-ACP
CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-
CC desaturase) gene in the seed of a cotton plant. The invention is useful
CC for producing cottonseed oil with reduced palmitic and/or linoleic acid
CC content, and increased stearic and/or oleic acid content. The present
CC DNA sequence is an oligonucleotide which is used for generating fatty
CC acid biosynthesis gene construct related to the invention.
XX
SQ Sequence 8 BP; 0 A; 3 C; 5 G; 0 U; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCGGGCC 9
|||||||
Db 7 CCGGGCC 1

RESULT 277
AAF20849/c
ID AAF20849 standard; DNA; 9 BP.
XX
AC AAF20849;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human adenosine A1 receptor polynucleotide fragment #2416.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 106; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with

CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 9 BP; 0 A; 3 C; 5 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCC 14
|||||||
Db 9 CCAGGCC 3

RESULT 278
AAA34727/c
ID AAA34727 standard; DNA; 9 BP.
XX
AC AAA34727;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2416.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 571; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 9 BP; 0 A; 3 C; 5 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCC 14'
|||||||
Db 9 CCAGGCC 3

RESULT 279
ABQ72098/c
ID ABQ72098 standard; DNA; 9 BP.
XX
AC ABQ72098;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2396.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -

```
XX
PS   Example 1; Page 61; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
CC   and specificity for their target sequences, as well as enhanced
CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC   represent DNA target sequences and zinc finger peptides which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 9 BP; 1 A; 2 C; 3 G; 3 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
               |||||||
Db          8 GCCAAAG 2


RESULT 280
ABQ72099/c
ID   ABQ72099 standard; DNA; 9 BP.
XX
AC   ABQ72099;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2397.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US43438.
XX
PR   20-NOV-2000; 2000US-0716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering,
PT   comprises first, second and third zinc fingers, ordered from N- to
PT   C-terminus  -
XX
PS   Example 1; Page 61; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
CC   and specificity for their target sequences, as well as enhanced
CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC   represent DNA target sequences and zinc finger peptides which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 9 BP; 1 A; 2 C; 3 G; 3 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
               |||||||
Db          8 GCCAAAG 2


RESULT 281
ABK95837/c
ID   ABK95837 standard; DNA; 10 BP.
XX
AC   ABK95837;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #8.
XX
KW   Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KW   glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KW   amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO200244198-A2.
XX
PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-US44781.
XX
PR   30-NOV-2000; 2000US-250254P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Kazemi A,  Russo DP,  Sausker EA;
XX
DR   WPI; 2002-519580/55.
XX
PT   Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT   Amino Acid Transporter), Member 4 isogenes, for improving efficiency
PT   and reliability in drug development for treating cancers -
XX
PS   Claim 17; Page 16; 139pp; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising a
CC   first nucleotide sequence which comprises solute carrier family 1
CC   (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
```

CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
CC which is a polymorphic variant of a reference sequence for SLC1A4
CC protein. Also described are methods for: (1) haplotyping or genotyping
CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
CC gene of an individual; (3) identifying an association between a trait and
CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful
CC in screening for drugs targeting (III) that are useful for treating
CC cancer, neurological diseases and amino acid transporter disorders. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with SLC1A4 activity. The haplotyping method is also
CC used by the pharmaceutical research scientist to validate SLC1A4 as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
CC and amino acid transporter disorders, and in the design of clinical
CC trials for treating a specific condition of disease associated with
CC SLC1A4 activity. The methods are also useful for screening compounds
CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
CC prognostic and therapeutic methods. ABK95761-ABK95877 represent
CC SLC1A4 gene allele-specific oligonucleotides, primer extension
CC oligonucleotides and related PCR primers used to identify single
CC nucleotide polymorphisms (SNP) of the gene.
XX
SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCC 14
|||||||
Db 10 CCAGGCC 4

RESULT 282
ABV63037/c
ID ABV63037 standard; cDNA; 11 BP.
XX
AC ABV63037;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 823.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 48; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGG 12
|||||||
Db 7 GGCCAGG 1

RESULT 283
ABV70458/c
ID ABV70458 standard; cDNA; 11 BP.
XX
AC ABV70458;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8244.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Claim 24; Page 264; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 11;

```
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGG 12
              |||||||
Db          7 GGCCAGG 1


RESULT 284
ABQ87161/c
ID   ABQ87161 standard; cDNA; 11 BP.
XX
AC   ABQ87161;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 916.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15178.
XX
PR   03-JAN-2001; 2001DE-1000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and ageing, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential
PT   gene expression  -
XX
PS   Claim 8; Page 75; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ   Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGG 12
              |||||||
Db          7 GGCCAGG 1


RESULT 285
AAS19877
ID   AAS19877 standard; DNA; 10 BP.
XX
AC   AAS19877;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Oligonucleotide #57 to detect human RANGAP1 gene polymorphisms.
XX
KW   Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KW   chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW   cancer; irregular cell cycle associated disorder; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179240-A2.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-US12455.
XX
PR   17-APR-2000; 2000US-198072P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-075068/10.
XX
PT   Genotyping human Ran GTPase activating protein 1 gene of individual for
PT   determining haplotype of individual, involves determining identity of
PT   nucleotide pair at specific polymorphic sites for two copies of the
PT   gene  -
XX
PS   Claim 17; Page 16; 148pp; English.
XX
CC   The present invention relates to novel single nucleotide polymorphisms
CC   (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC   located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC   genotyping the RANGAP1 gene. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC   primer-extension oligonucleotides for detecting the RANGAP1 gene
CC   polymorphisms. The polynucleotides and screened compounds are useful for
CC   treatment of diseases associated with RANGAP1 activity, such as
CC   cancer and other disorders associated with an irregular cell cycle.
CC   AAS19821-AAS19898 represent primer-extension oligonucleotides for
CC   detecting human RANGAP1 gene polymorphisms.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||| |||| |
Db          1 TCCTGGCCCG 10


RESULT 286
AAX18625
ID   AAX18625 standard; DNA; 10 BP.
XX
AC   AAX18625;
XX
DT   06-MAY-1999  (first entry)
XX
DE   p53 serial analysis of gene expression tag #9.
XX
KW   p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic;
KW   rat embryo fibroblast; REF; tumour suppressor; cell cycle control;
KW   tumourigenesis; diagnosis; ss.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   WO9901581-A1.
XX
PD   14-JAN-1999.
XX
```

```
PF   02-JUL-1998;   98WO-US13903.
XX
PR   02-JUL-1997;   97US-0051573.
XX
PA   (GENZ ) GENZYME CORP.
XX
PI   Beaudry GA,  Bertelsen AH,  Galella EA,  Madden SL;
XX
DR   WPI; 1999-106079/09.
XX
PT   Diagnosis of cancer in potentially neoplastic samples - by comparing
PT   the level of transcription between RNA transcripts in two tissue
PT   samples, useful for providing an extensive profile of gene
PT   expression in rat embryo fibroblast (REF) cells
XX
PS   Example 2; Page 15; 32pp; English.
XX
CC   A method has been developed for the diagnosis of cancer in potentially
CC   neoplastic samples. The method comprises comparing the level of
CC   transcription between RNA transcripts in two tissue samples (which are
CC   of the same type), where the first sample is potentially neoplastic, and
CC   the second sample is normal human tissue. The first sample is
CC   categorized as neoplastic if its level of transcription is lower than
CC   that of the second sample. The transcript is selected from Alu, RAS,
CC   U6 snRNA, 16S RNA, EGR-1, ribosomal protein S27, ETS-1, 28S RNA, CGR11,
CC   and LIMK-2, and it is identified by a tag selected from ribosomal
CC   protein L13a, alpha-tubulin (T1) and (T2), thymosin beta-4, and gamma-
CC   actin. The present sequence represents a serial analysis of gene
CC   expression (SAGE) tag from the present invention. The use of SAGE tags
CC   provides an extensive profile of gene expression in rat embryo
CC   fibroblast (REF) cells containing the (non)-functional p53 tumour
CC   suppression gene. The discovery of new SAGE tags, which are regulated
CC   by p53, enables the diagnosis of genes that are related to cell cycle
CC   control and tumourigenesis.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              |||| ||| |
Db          1 GGCCTGGCTA 10


RESULT 287
AAZ79322
ID   AAZ79322 standard; DNA; 10 BP.
XX
AC   AAZ79322;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1750.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 115; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;
```

```
  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||  ||| 
Db          1 CAGGCCTGGC 10


RESULT 288
AAZ83064/c
ID   AAZ83064 standard; DNA; 10 BP.
XX
AC   AAZ83064;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2298.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 121; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAA 17
              || ||||  || 
Db         10 CCTGGCCCAA 1


RESULT 289
AAZ83855/c
ID   AAZ83855 standard; DNA; 10 BP.
XX
AC   AAZ83855;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3089.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 141; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
```

```
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| || |||
Db         10 GCCCGGACAA 1


RESULT 290
AAZ85316
ID   AAZ85316 standard; DNA; 10 BP.
XX
AC   AAZ85316;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4550.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 181; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | |||| |||
Db          1 CAGGCCTGGC 10


RESULT 291
AAH64036
ID   AAH64036 standard; cDNA; 10 BP.
XX
AC   AAH64036;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 876.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 59; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | |||| |||
Db          1 CAGGCCTGGC 10


RESULT 292
AAH64037
```

```
ID   AAH64037 standard; cDNA; 10 BP.
XX
AC   AAH64037;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 877.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 59; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||  |||
Db          1 CAGGCCTGGC 10


RESULT 293
AAX55034
ID   AAX55034 standard; DNA; 11 BP.
XX
AC   AAX55034;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74.. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || ||||  ||
Db          2 CCCGGCCCGG 11


RESULT 294
AAF20603
ID   AAF20603 standard; DNA; 11 BP.
XX
AC   AAF20603;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2170.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
```

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

Query Match 34.0%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGGGCCAGG 12
|| |||| ||
Db 2 CCCGGCCCGG 11

RESULT 295
AAA34481
ID AAA34481 standard; DNA; 11 BP.
XX
AC AAA34481;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2170.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 537; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

Query Match 34.0%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGGGCCAGG 12
|| |||| ||
Db 2 CCCGGCCCGG 11

```
RESULT 296
ABV68762
ID   ABV68762 standard; cDNA; 11 BP.
XX
AC   ABV68762;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6548.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 207; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 other;

  Query Match            34.0%;  Score 6.8;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              |||| | |||
Db          2 GGCCTGCCCA 11


RESULT 297
AAX55033
ID   AAX55033 standard; DNA; 12 BP.
XX
AC   AAX55033;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;

  Query Match            34.0%;  Score 6.8;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || |||| ||
Db          3 CCCGGCCCGG 12


RESULT 298
AAF20602
ID   AAF20602 standard; DNA; 12 BP.
XX
AC   AAF20602;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2169.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
```

```
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 264; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || |||| ||
Db          3 CCCGGCCCGG 12
```

```
RESULT 299
AAA34480
ID   AAA34480 standard; DNA; 12 BP.
XX
AC   AAA34480;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2169.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 537; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
```

```
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              || |||| ||
Db          3 CCCGGCCCGG 12


RESULT 300
AAX29560
ID   AAX29560 standard; DNA; 8 BP.
XX
AC   AAX29560;
XX
DT   03-JUN-1999  (first entry)
XX
DE   Primer for human G-protein coupled receptor genes.
XX
KW   Nucleic acid amplification; nuclear receptor; G-protein coupled receptor;
KW   apoptosis; DNA repair; DNA replication; plant biology; agriculture;
KW   human; veterinary medicine; reproduction; microbiology; hybridisation;
KW   environmental science; DNA fingerprinting; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9911823-A2.
XX
PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US18392.
XX
PR   05-SEP-1997;   97US-0925816.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   McClelland M,  Pesole G;
XX
DR   WPI; 1999-205200/17.
XX
PT   Subset of primers able to amplify group of related sequences
XX
PS   Claim 21; Page 75; 92pp; English.
XX
CC   The invention provides primers (AAX29501-X29679) for identifying
CC   sequences encoding structurally or functionally related proteins such as
CC   nuclear or G-protein coupled receptors, apoptosis-related or DNA
CC   repair/replication proteins. The identified sequences are broadly useful
CC   in plant biology, agriculture, human or veterinary medicine,
CC   reproduction, microbiology or environmental science, e.g. to study
CC   expression of nuclear receptors at different stages of tissue development
CC   or after treatment with particular drugs. It is also used for DNA
CC   fingerprinting (to generate products useful for differential
CC   hybridisation), or, where a 3'-anchor primer is used, to isolate the
CC   3'-ends of mRNA sequences. Sequences AAX29526-X29583 represent claimed
CC   primers specific for human G-protein coupled receptor genes.
XX
SQ   Sequence 8 BP; 0 A; 4 C; 2 G; 2 T; 0 other;

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5.8e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCC 9
              ||| ||||
Db          1 TCCTGGCC 8


Search completed: November 10, 2003, 08:01:33
Job time : 2 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 08:03:58 ; Search time 0.001 Seconds
(without alignments)
34.200 Million cell updates/sec

Title: us-09-774-809-31
Perfect score: 20
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 69 seqs, 855 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 84 summaries

Database : rni.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	US-08-910-629A-31	Sequence 31, Appl
c	2	20	100.0	20	1	US-08-910-629A-42	Sequence 42, Appl
	3	20	100.0	20	1	US-09-209-668-7	Sequence 7, Appli
	4	20	100.0	20	1	US-09-287-796-31	Sequence 31, Appl
c	5	20	100.0	20	1	US-09-287-796-42	Sequence 42, Appl
	6	20	100.0	20	1	US-09-130-616-31	Sequence 31, Appl
c	7	20	100.0	20	1	US-09-130-616-42	Sequence 42, Appl
c	8	15.4	77.0	17	1	US-09-371-772B-6740	Sequence 6740, Ap
	9	15.4	77.0	18	1	US-08-951-923-51	Sequence 51, Appl
c	10	14.8	74.0	18	1	US-08-584-040-6244	Sequence 6244, Ap
c	11	14.8	74.0	18	1	US-09-371-772B-3004	Sequence 3004, Ap
c	12	14.4	72.0	17	1	US-08-584-040-4222	Sequence 4222, Ap
c	13	14.4	72.0	17	1	US-09-371-772B-1989	Sequence 1989, Ap
c	14	14	70.0	17	1	US-08-584-040-7661	Sequence 7661, Ap
c	15	14	70.0	17	1	US-09-371-772B-3450	Sequence 3450, Ap
c	16	13.8	69.0	17	1	US-09-371-772B-4833	Sequence 4833, Ap
c	17	13.4	67.0	16	1	US-09-371-772B-5851	Sequence 5851, Ap
	18	13.4	67.0	17	1	US-08-924-183-6	Sequence 6, Appli
	19	13.4	67.0	17	1	US-09-488-364-6	Sequence 6, Appli
c	20	13.4	67.0	17	1	US-08-584-040-1996	Sequence 1996, Ap
c	21	13.4	67.0	17	1	US-09-371-772B-541	Sequence 541, App
c	22	13.4	67.0	17	1	US-09-371-772B-4834	Sequence 4834, Ap
c	23	13	65.0	17	1	US-08-584-040-7660	Sequence 7660, Ap
c	24	13	65.0	17	1	US-09-371-772B-3449	Sequence 3449, Ap
c	25	12.8	64.0	17	1	US-08-584-040-5795	Sequence 5795, Ap
c	26	12.8	64.0	17	1	US-09-371-772B-2661	Sequence 2661, Ap
c	27	10.4	52.0	12	1	US-08-822-586-49	Sequence 49, Appl
	28	10.4	52.0	12	1	US-09-281-418-100	Sequence 100, App
c	29	9.8	49.0	13	1	US-08-882-046-77	Sequence 77, Appl
	30	9.8	49.0	13	1	US-09-922-445-11	Sequence 11, Appl
c	31	9.8	49.0	13	1	US-09-922-445-36	Sequence 36, Appl
	32	9.4	47.0	11	1	US-09-249-155A-324	Sequence 324, App
c	33	8.8	44.0	18	1	US-08-951-923-51	Sequence 51, Appl
	34	8.4	42.0	10	1	US-08-388-353-387	Sequence 387, App
	35	8.4	42.0	10	1	US-08-488-551B-387	Sequence 387, App
c	36	8.4	42.0	10	1	US-08-522-384-63	Sequence 63, Appl
	37	8.4	42.0	10	1	US-09-720-201A-24	Sequence 24, Appl
	38	8.4	42.0	12	1	US-08-822-586-49	Sequence 49, Appl
	39	8	40.0	8	1	US-08-859-954-105	Sequence 105, App
c	40	8	40.0	10	1	US-08-441-887A-183	Sequence 183, App
c	41	8	40.0	10	1	US-08-192-942-6	Sequence 6, Appli
	42	8	40.0	10	1	US-08-388-353-388	Sequence 388, App
	43	8	40.0	10	1	US-08-388-353-389	Sequence 389, App
	44	8	40.0	10	1	US-08-488-551B-388	Sequence 388, App
	45	8	40.0	10	1	US-08-488-551B-389	Sequence 389, App
c	46	7.8	39.0	17	1	US-08-924-183-6	Sequence 6, Appli
c	47	7.8	39.0	17	1	US-09-488-364-6	Sequence 6, Appli
c	48	7.6	38.0	20	1	US-08-910-629A-31	Sequence 31, Appl
	49	7.6	38.0	20	1	US-08-910-629A-42	Sequence 42, Appl
c	50	7.6	38.0	20	1	US-09-209-668-7	Sequence 7, Appli
c	51	7.6	38.0	20	1	US-09-287-796-31	Sequence 31, Appl
	52	7.6	38.0	20	1	US-09-287-796-42	Sequence 42, Appl
c	53	7.6	38.0	20	1	US-09-130-616-31	Sequence 31, Appl
	54	7.6	38.0	20	1	US-09-130-616-42	Sequence 42, Appl
	55	7	35.0	8	1	US-08-105-483-423	Sequence 423, App
	56	7	35.0	8	1	US-08-709-209-423	Sequence 423, App
	57	7	35.0	8	1	US-08-303-275-131	Sequence 131, App
	58	7	35.0	8	1	US-08-458-101-423	Sequence 423, App
	59	7	35.0	8	1	US-08-859-954-106	Sequence 106, App
	60	7	35.0	8	1	US-08-859-954-359	Sequence 359, App
c	61	6.4	32.0	8	1	US-08-474-700B-43	Sequence 43, Appl
	62	6.4	32.0	8	1	US-08-859-954-56	Sequence 56, Appl
	63	6.4	32.0	8	1	US-08-859-954-107	Sequence 107, App
c	64	6.4	32.0	8	1	US-09-041-675-9	Sequence 9, Appli
	65	6.4	32.0	8	1	US-09-041-675-15	Sequence 15, Appl
	66	6.4	32.0	8	1	US-09-041-675-23	Sequence 23, Appl
	67	6.4	32.0	8	1	US-08-646-301A-10	Sequence 10, Appl
c	68	6.4	32.0	8	1	US-08-646-301A-10	Sequence 10, Appl
c	69	6.4	32.0	8	1	US-09-398-499-16	Sequence 16, Appl
	70	6.4	32.0	8	1	US-09-398-499-39	Sequence 39, Appl
	71	6.4	32.0	10	1	US-08-522-384-63	Sequence 63, Appl
	72	6.4	32.0	17	1	US-08-584-040-7661	Sequence 7661, Ap
	73	6.4	32.0	17	1	US-09-371-772B-3450	Sequence 3450, Ap
c	74	6	30.0	8	1	US-07-949-541A-34	Sequence 34, Appl
c	75	6	30.0	8	1	US-07-949-541A-39	Sequence 39, Appl
c	76	6	30.0	8	1	US-08-593-345B-13	Sequence 13, Appl
c	77	6	30.0	8	1	US-08-859-954-53	Sequence 53, Appl
c	78	6	30.0	8	1	US-08-859-954-81	Sequence 81, Appl
	79	6	30.0	8	1	US-08-859-954-104	Sequence 104, App
c	80	6	30.0	8	1	US-08-859-954-329	Sequence 329, App
	81	6	30.0	8	1	US-08-859-954-332	Sequence 332, App
c	82	6	30.0	8	1	US-08-859-954-333	Sequence 333, App
	83	6	30.0	8	1	US-08-859-954-360	Sequence 360, App
	84	6	30.0	8	1	US-08-859-954-396	Sequence 396, App

ALIGNMENTS

RESULT 1
US-08-910-629A-31
; Sequence 31, Application US/08910629A
; Patent No. 5877309
; GENERAL INFORMATION:
; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; APPLICANT: Brett Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITONS AND METHODS FOR THE MODULATION OF JNK
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ

```
;       COUNTRY:  USA
;       ZIP:  08053
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 MB
;       MEDIUM TYPE:  STORAGE
;       COMPUTER:  PENTIUM
;       OPERATING SYSTEM:  WINDOWS 95
;       SOFTWARE:  WORDPERFECT 6.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/910,629A
;       FILING DATE:  August 13, 1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  ISPH-0215
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609) 779-2400
;       TELEFAX:  (609) 779-8488
;   INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
;     ANTI-SENSE:  Yes
US-08-910-629A-31

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 2
US-08-910-629A-42/c
; Sequence 42, Application US/08910629A
; Patent No. 5877309
;  GENERAL INFORMATION:
;     APPLICANT:  Robert A. McKay
;     APPLICANT:  Nicholas M. Dean
;     APPLICANT:  Brett Monia
;     TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDE
;     TITLE OF INVENTION:  COMPOSITONS AND METHODS FOR THE MODULATION OF JNK
;     TITLE OF INVENTION:  PROTEINS
;     NUMBER OF SEQUENCES:  86
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Law Offices of Jane Massey Licata
;       STREET:  66 East Main Street
;       CITY:  Marlton
;       STATE:  NJ
;       COUNTRY:  USA
;       ZIP:  08053
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 MB
;       MEDIUM TYPE:  STORAGE
;       COMPUTER:  PENTIUM
;       OPERATING SYSTEM:  WINDOWS 95
;       SOFTWARE:  WORDPERFECT 6.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/910,629A
;       FILING DATE:  August 13, 1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  ISPH-0215
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609) 779-2400
;       TELEFAX:  (609) 779-8488
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
;     ANTI-SENSE:  No
US-08-910-629A-42

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db         20 GTCCGGGCCAGGCCAAAGTC 1


RESULT 3
US-09-209-668-7
; Sequence 7, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
;  TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
;  FILE REFERENCE: ISPH-0336
;  CURRENT APPLICATION NUMBER: US/09/209,668A
;  CURRENT FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-209-668-7

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 4
US-09-287-796-31
; Sequence 31, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0350
;  CURRENT APPLICATION NUMBER: US/09/287,796A
;  CURRENT FILING DATE: 1999-04-07
;  EARLIER APPLICATION NUMBER: 09/130,616
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
```

```
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-287-796-31

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 5
US-09-287-796-42/c
; Sequence 42, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0350
;  CURRENT APPLICATION NUMBER: US/09/287,796A
;  CURRENT FILING DATE: 1999-04-07
;  EARLIER APPLICATION NUMBER: 09/130,616
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-287-796-42

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db         20 GTCCGGGCCAGGCCAAAGTC 1


RESULT 6
US-09-130-616-31
; Sequence 31, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0318
;  CURRENT APPLICATION NUMBER: US/09/130,616C
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-130-616-31

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 7
US-09-130-616-42/c
; Sequence 42, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0318
;  CURRENT APPLICATION NUMBER: US/09/130,616C
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-130-616-42

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db         20 GTCCGGGCCAGGCCAAAGTC 1


RESULT 8
US-09-371-772B-6740/c
; Sequence 6740, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
```

```
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6740
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-6740

  Query Match             77.0%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 4;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAGT 19
              ||||||| |||||||
Db         17 CCGGGCCAAGCCAAAGT 1


RESULT 9
US-08-951-923-51
; Sequence 51, Application US/08951923
; Patent No. 6048693
;  GENERAL INFORMATION:
;    APPLICANT:  Bitter, Grant
;    TITLE OF INVENTION:  PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE
;    TITLE OF INVENTION:  FUNCTION
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward LLP
;      STREET:  5 Palo Alto Square, 3000 El Camino Real
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/951,923
;      FILING DATE:  October 16, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Neeley, Richard L.
;      REGISTRATION NUMBER:  30,092
;      REFERENCE/DOCKET NUMBER:  BITT-001/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650 843-5000
;      TELEFAX:  650 857-0663
;      TELEX:  380816COOLEYPA
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:.  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-951-923-51

  Query Match             77.0%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 4.4;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCCAAAGTC 20
              | ||||||||||||||||
Db          2 CTGGCCAGGCCAAAGTC 18


RESULT 10
US-08-584-040-6244/c
; Sequence 6244, Application US/08584040
; Patent No. 6346398 ,       ,
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  6244:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-6244

  Query Match             74.0%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 5.5;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAGTC 20
              |||||||| ||| |||||
Db         18 CCGGGCCAAGCCGAAGTC 1


RESULT 11
US-09-371-772B-3004/c
; Sequence 3004, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
```

```
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3004
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-3004

  Query Match             74.0%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 5.5;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAGTC 20
              |||||||| ||| |||||
Db         18 CCGGGCCAAGCCGAAGTC 1


RESULT 12
US-08-584-040-4222/c
; Sequence 4222, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4222:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-4222

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 5.9;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              |||||||| |||||||
Db         16 CCGGGCCAAGCCAAAG 1


RESULT 13
US-09-371-772B-1989/c
; Sequence 1989, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1989
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1989

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 5.9;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              |||||||| |||||||
Db         16 CCGGGCCAAGCCAAAG 1


RESULT 14
US-08-584-040-7661/c
; Sequence 7661, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7661:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-7661

  Query Match             70.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.9;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAAAGTC 20
              ||||||||||||||
Db         17 GCCAGGCCAAAGTC 4


RESULT 15
US-09-371-772B-3450/c
; Sequence 3450, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3450
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-3450

  Query Match             70.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.9;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAAAGTC 20
              ||||||||||||||
Db         17 GCCAGGCCAAAGTC 4


RESULT 16
US-09-371-772B-4833/c
; Sequence 4833, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4833
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-4833

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAGT 19
              ||||||  |||||||| |
Db         17 CCGGGCAAGGCCAAAAT 1


RESULT 17
US-09-371-772B-5851/c
; Sequence 5851, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5851
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-5851

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 8;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAA 17
              ||||||  ||||||||
Db         16 CCGGGCAAGGCCAAA 2


RESULT 18
US-08-924-183-6
; Sequence 6, Application US/08924183A
; Patent No. 6218109
; GENERAL INFORMATION:
;  APPLICANT: Elledge, Stephen J.
```

```
;  APPLICANT: Sanchez, Yolanda
;  TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
;  FILE REFERENCE: 120541-1003
;  CURRENT APPLICATION NUMBER: US/08/924,183A
;  CURRENT FILING DATE: 1997-09-05
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-08-924-183-6

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 8.8;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              || ||||||||||||
Db          3 GGACAGGCCAAAGTC 17


RESULT 19
US-09-488-364-6
; Sequence 6, Application US/09488364
; Patent No. 6307015
; GENERAL INFORMATION:
;  APPLICANT: Elledge, Stephen J.
;  APPLICANT: Sanchez, Yolanda
;  TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
;  FILE REFERENCE: 120541-1013
;  CURRENT APPLICATION NUMBER: US/09/488,364
;  CURRENT FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-488-364-6

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 8.8;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              || ||||||||||||
Db          3 GGACAGGCCAAAGTC 17


RESULT 20
US-08-584-040-1996/c
; Sequence 1996, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;      APPLICANT:  Pavco, Pamela
;      APPLICANT:  McSwiggen, James
;      APPLICANT:  Stinchcomb, Dan T.
;      APPLICANT:  Escobedo, Jaime
;      TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;      TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;      TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;      TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;      TITLE OF INVENTION:  GROWTH FACTOR
;      NUMBER OF SEQUENCES:  8502
;      CORRESPONDENCE ADDRESS:
;        ADDRESSEE:  Lyon & Lyon
;        STREET:  633 West Fifth Street
;        STREET:  Suite 4700
;        CITY:  Los Angeles
;        STATE:  California
;        COUNTRY:  U.S.A.
;        ZIP:  90071-2066
;      COMPUTER READABLE FORM:
;        MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;        MEDIUM TYPE:  storage
;        COMPUTER:  IBM Compatible
;        OPERATING SYSTEM:  IBM P.C. DOS 5.0
;        SOFTWARE:  Word Perfect 5.1
;      CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/584,040
;        FILING DATE:  January 11, 1996
;        CLASSIFICATION:  514
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  60/005,974
;        FILING DATE:  October 26, 1995
;      ATTORNEY/AGENT INFORMATION:
;        NAME:  Warburg, Richard J.
;        REGISTRATION NUMBER:  32,327
;        REFERENCE/DOCKET NUMBER:  218/064
;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  (213) 489-1600
;        TELEFAX:  (213) 955-0440
;        TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1996:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  17 base pairs
;        TYPE:  nucleic acid
;        STRANDEDNESS:  single
;        TOPOLOGY:  linear
US-08-584-040-1996

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 8.8;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAA 17
              |||||| ||||||||
Db         15 CCGGGCAAGGCCAAA 1


RESULT 21
US-09-371-772B-541/c
; Sequence 541, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 541
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-541

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 8.8;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          3 CCGGGCCAGGCCAAA 17
              |||||| ||||||||
Db         15 CCGGGCAAGGCCAAA 1


RESULT 22
US-09-371-772B-4834/c
; Sequence 4834, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4834
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-4834

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 8.8;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAA 17
              |||||| ||||||||
Db         16 CCGGGCAAGGCCAAA 2


RESULT 23
US-08-584-040-7660/c
; Sequence 7660, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7660:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-7660

  Query Match             65.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAAGTC 20
              |||||||||||||
Db         17 CCAGGCCAAAGTC 5


RESULT 24
US-09-371-772B-3449/c
; Sequence 3449, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3449
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-3449

  Query Match             65.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCAAAGTC 20
              |||||||||||||
Db         17 CCAGGCCAAAGTC 5


RESULT 25
US-08-584-040-5795/c
; Sequence 5795, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
```

```
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5795:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-5795

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 11;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              ||||||||  |||  |||
Db         16 CCGGGCCAAGCCGAAG 1


RESULT 26
US-09-371-772B-2661/c
; Sequence 2661, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2661
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-2661

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 11;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAG 18
              ||||||||  |||  |||
Db         16 CCGGGCCAAGCCGAAG 1


RESULT 27
US-08-822-586-49/c
; Sequence 49, Application US/08822586
; Patent No. 6015890
;  GENERAL INFORMATION:
;    APPLICANT:  WIILIAM R. JACOBS, JR., JAMES M. MUSSER AND
;    APPLICANT:  AMALIO TELENTI
;    TITLE OF INVENTION:  AN EMBCAB OPERON OF MYCOBACTERIA AND
;    TITLE OF INVENTION:  MUTANTS THEREOF
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMSTER, ROTHSTEIN & EBENSTEIN
;      STREET:  90 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH 1.44 Mb STORAGE
;      MEDIUM TYPE:  DISKETTE
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,586
;      FILING DATE:  MARCH 20, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ELIZABETH A. BOGOSIAN
;      REGISTRATION NUMBER:  39,911
;      REFERENCE/DOCKET NUMBER:  96700/437
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 697-5995
;      TELEFAX:  (212) 286-0854 or 286-0082
;      TELEX:  TWX 710-581-4766
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  NO
US-08-822-586-49

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 17;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCCAA 16
              ||||||||||  |
Db         12 GGGCCAGGCCCA 1


RESULT 28
US-09-281-418-100
; Sequence 100, Application US/09281418
; Patent No. 6287769
```

```
; GENERAL INFORMATION:
;  APPLICANT: Inoue, Takakazu
;  TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
;  TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
;  TITLE OF INVENTION: nisms and Method of Assaying Contaminant
;  FILE REFERENCE: 9982-7
;  CURRENT APPLICATION NUMBER: US/09/281,418
;  CURRENT FILING DATE: 1999-03-30
;  EARLIER APPLICATION NUMBER: JP/1998/87651
;  EARLIER FILING DATE: 1998-03-31
;  EARLIER APPLICATION NUMBER: JP/1999/69694
;  EARLIER FILING DATE: 1999-03-16
;  NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 100
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-281-418-100

  Query Match           52.0%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 17;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAAAGTC 20
              |||||| |||||
Db          1 CAGGCCGAAGTC 12


RESULT 29
US-08-882-046-77/c
; Sequence 77, Application US/08882046
; Patent No. 6136952
;  GENERAL INFORMATION:
;    APPLICANT:  Li, Linheng
;    APPLICANT:  Hood, Leroy
;    APPLICANT:  Krantz, Ian D.
;    APPLICANT:  Spinner, Nancy B.
;    TITLE OF INVENTION:  Human Jagged Polypeptide, Encoding
;    TITLE OF INVENTION:  Nucleic Acids and Methods of Use
;    NUMBER OF SEQUENCES:  110
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/882,046
;      FILING DATE:  25-JUN-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UW 2637
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  77:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-882-046-77

  Query Match           49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 23;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCCAAA 17
              |||||| |||| |
Db         13 GGGCCACGCCACA 1


RESULT 30
US-09-922-445-11
; Sequence 11, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
;  APPLICANT: Andersson, Maria K.
;  APPLICANT:  Berglund, Lars G. T.
;  APPLICANT:  Reneland, Rikard  H.
;  APPLICANT:  Adam, Gail I. R.
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
;  FILE REFERENCE: GG126US
;  CURRENT APPLICATION NUMBER: US/09/922,445
;  CURRENT FILING DATE:  2001-08-03
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: synthetic
US-09-922-445-11

  Query Match           49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 23;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCA 15
              |||  ||||||||
Db          1 CCGACCCAGGCCA 13


RESULT 31
US-09-922-445-36/c
; Sequence 36, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
;  APPLICANT: Andersson, Maria K.
;  APPLICANT:  Berglund, Lars G. T.
;  APPLICANT:  Reneland, Rikard  H.
;  APPLICANT:  Adam, Gail I. R.
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
;  FILE REFERENCE: GG126US
;  CURRENT APPLICATION NUMBER: US/09/922,445
;  CURRENT FILING DATE:  2001-08-03
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: synthetic
US-09-922-445-36

  Query Match           49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 23;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCA 15
              |||  ||||||||
Db         13 CCGACCCAGGCCA 1


RESULT 32
US-09-249-155A-324
; Sequence 324, Application US/09249155A
; Patent No. 6538173
```

```
; GENERAL INFORMATION:
;  APPLICANT:  Heber-Katz, Ellen
;  TITLE OF INVENTION:  Compositions and Methods for Wound
;  TITLE OF INVENTION:  Healing
;  FILE REFERENCE:  00486.78503
;  CURRENT APPLICATION NUMBER: US/09/249,155A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER:  US 60/074,737
;  PRIOR FILING DATE:  1998-02-13
;  PRIOR APPLICATION NUMBER:  US 60/097,937
;  PRIOR FILING DATE:  1998-08-26
;  PRIOR APPLICATION NUMBER:  US 60/102,051
;  PRIOR FILING DATE:  1998-09-28
;  NUMBER OF SEQ ID NOS:  346
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 324
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-249-155A-324

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 22;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAGG 12
              ||||||| |||
Db          1 TCCGGGCGAGG 11


RESULT 33
US-08-951-923-51/c
; Sequence 51, Application US/08951923
; Patent No. 6048693
;  GENERAL INFORMATION:
;    APPLICANT:  Bitter, Grant
;    TITLE OF INVENTION:  PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE
;    TITLE OF INVENTION:  FUNCTION
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward LLP
;      STREET:  5 Palo Alto Square, 3000 El Camino Real
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/951,923
;      FILING DATE:  October 16, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Neeley, Richard L.
;      REGISTRATION NUMBER:  30,092
;      REFERENCE/DOCKET NUMBER:  BITT-001/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650 843-5000
;      TELEFAX:  650 857-0663
;      TELEX:  380816COOLEYPA
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-951-923-51

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 43;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAA 17
              |||| ||||| |
Db         12 GGCCTGGCCAGA 1


RESULT 34
US-08-388-353-387
; Sequence 387, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  387:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-387

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              | ||||||||
Db          1 CAGGGCCAGG 10


RESULT 35
US-08-488-551B-387
; Sequence 387, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
```

```
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  387:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-387

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGG 12
              | ||||||||
Db          1 CAGGGCCAGG 10


RESULT 36
US-08-522-384-63/c
; Sequence 63, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
;  APPLICANT: LOPEZ-NIETO, CARLOS E
;  APPLICANT: NIGAM, SANJAY KUMAR
;  TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
;  TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 2458-4029
;  CURRENT APPLICATION NUMBER: US/08/522,384
;  CURRENT FILING DATE: 1996-11-15
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:  Primer
US-08-522-384-63

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||||||
Db         10 CAGGCCAGGC 1


RESULT 37
US-09-720-201A-24
; Sequence 24, Application US/09720201A
; Patent No. 6524853
; GENERAL INFORMATION:
;  APPLICANT: KOHARA, MICHINORI
;  APPLICANT:  KOHARA, KYOKO
;  APPLICANT:  TAIRA, KAZUNARI
;  APPLICANT:  MATSUZAKI, JUNICHI
;  APPLICANT:  OHMORI, HIROSHI
;  TITLE OF INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH GENE AND
;  TITLE OF INVENTION:  ITS USE
;  FILE REFERENCE: 04853.0051-00000
;  CURRENT APPLICATION NUMBER: US/09/720,201A
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: JP 98/177,820
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: PCT/JP99/03381
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-720-201A-24

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||||||| ||
Db          1 GGGCCAGCCC 10


RESULT 38
US-08-822-586-49
; Sequence 49, Application US/08822586
; Patent No. 6015890
;  GENERAL INFORMATION:
;    APPLICANT:  WIILIAM R. JACOBS, JR., JAMES M. MUSSER AND
;    APPLICANT:  AMALIO TELENTI
;    TITLE OF INVENTION:  AN EMBCAB OPERON OF MYCOBACTERIA AND
;    TITLE OF INVENTION:  MUTANTS THEREOF
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMSTER, ROTHSTEIN & EBENSTEIN
;      STREET:  90 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH 1.44 Mb STORAGE
;      MEDIUM TYPE:  DISKETTE
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,586
;      FILING DATE:  MARCH 20, 1997
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ELIZABETH A. BOGOSIAN
;      REGISTRATION NUMBER:  39,911
;      REFERENCE/DOCKET NUMBER:  96700/437
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 697-5995
;      TELEFAX:  (212) 286-0854 or 286-0082
;      TELEX:  TWX 710-581-4766
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  NO
US-08-822-586-49

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity  90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              ||||| ||||
Db          2 GGGCCTGGCC 11


RESULT 39
US-08-859-954-105
; Sequence 105, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-105

  Query Match            40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAGT 19
              ||||||||
Db          1 GCCAAAGT 8


RESULT 40
US-08-441-887A-183/c
; Sequence 183, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;    APPLICANT:  Chee, Mark
;    APPLICANT:  Cronin, Maureen T.
;    APPLICANT:  Fodor, Stephen P.A.
;    APPLICANT:  Huang, Xiaohua X.
;    APPLICANT:  Hubbell, Earl A.
;    APPLICANT:  Lipshutz, Robert J.
;    APPLICANT:  Lobban, Peter E.
;    APPLICANT:  Morris, Macdonald S.
;    APPLICANT:  Sheldon, Edward L.
;    TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;    TITLE OF INVENTION:  Biological Chips
;    NUMBER OF SEQUENCES:  360
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,887A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/143,312
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/082,937
;      FILING DATE:  25-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  018547-004160US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-326-2400
;      TELEFAX:  650-326-2422
;  INFORMATION FOR SEQ ID NO:  183:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (probe)
US-08-441-887A-183

  Query Match            40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 32;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCC 9
```

```
                  ||||||||
Db          8 TCCGGGCC 1


RESULT 41
US-08-192-942-6/c
; Sequence 6, Application US/08192942
; Patent No. 5989906
;  GENERAL INFORMATION:
;    APPLICANT:  JAMES D. THOMPSON
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING P-GLYCOPROTEIN mdr-
;    TITLE OF INVENTION:  1 GENE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM COMPATIBLE
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,942
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/882,885
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  197/173
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-192-942-6

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 GCCAAAGT 19
               ||||||||
Db          10 GCCAAAGT 3


RESULT 42
US-08-388-353-388
; Sequence 388, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  388:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-388

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           5 GGGCCAGG 12
               ||||||||
Db           2 GGGCCAGG 9


RESULT 43
US-08-388-353-389
; Sequence 389, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
```

```
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  389:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-389

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          1 GGGCCAGG 8


RESULT 44
US-08-488-551B-388
; Sequence 388, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  388:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-388

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          2 GGGCCAGG 9


RESULT 45
US-08-488-551B-389
; Sequence 389, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  389:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-389

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          1 GGGCCAGG 8


RESULT 46
US-08-924-183-6/c
; Sequence 6, Application US/08924183A
; Patent No. 6218109
; GENERAL INFORMATION:
;  APPLICANT: Elledge, Stephen J.
```

```
;  APPLICANT: Sanchez, Yolanda
;  TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
;  FILE REFERENCE: 120541-1003
;  CURRENT APPLICATION NUMBER: US/08/924,183A
;  CURRENT FILING DATE: 1997-09-05
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-08-924-183-6

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 47
US-09-488-364-6/c
; Sequence 6, Application US/09488364
; Patent No. 6307015
; GENERAL INFORMATION:
;  APPLICANT: Elledge, Stephen J.
;  APPLICANT: Sanchez, Yolanda
;  TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
;  FILE REFERENCE: 120541-1013
;  CURRENT APPLICATION NUMBER: US/09/488,364
;  CURRENT FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-488-364-6

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 48
US-08-910-629A-31/c
; Sequence 31, Application US/08910629A
; Patent No. 5877309
;  GENERAL INFORMATION:
;    APPLICANT:  Robert A. McKay
;    APPLICANT:  Nicholas M. Dean
;    APPLICANT:  Brett Monia
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  COMPOSITONS AND METHODS FOR THE MODULATION OF JNK
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Jane Massey Licata
;      STREET:  66 East Main Street
;      CITY:  Marlton
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 MB
;      MEDIUM TYPE:  STORAGE
;      COMPUTER:  PENTIUM
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WORDPERFECT 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,629A
;      FILING DATE:  August 13, 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  ISPH-0215
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  Yes
US-08-910-629A-31

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 55;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 49
US-08-910-629A-42
; Sequence 42, Application US/08910629A
; Patent No. 5877309
;  GENERAL INFORMATION:
;    APPLICANT:  Robert A. McKay
;    APPLICANT:  Nicholas M. Dean
;    APPLICANT:  Brett Monia
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  COMPOSITONS AND METHODS FOR THE MODULATION OF JNK
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Jane Massey Licata
;      STREET:  66 East Main Street
;      CITY:  Marlton
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 MB
;      MEDIUM TYPE:  STORAGE
;      COMPUTER:  PENTIUM
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WORDPERFECT 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,629A
;      FILING DATE:  August 13, 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
```

```
;       REFERENCE/DOCKET NUMBER:  ISPH-0215
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609) 779-2400
;       TELEFAX:  (609) 779-8488
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
;     ANTI-SENSE:  No
US-08-910-629A-42

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 55;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db          7 GGCCTGGCCCGGAC 20


RESULT 50
US-09-209-668-7/c
; Sequence 7, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
;  TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
;  FILE REFERENCE: ISPH-0336
;  CURRENT APPLICATION NUMBER: US/09/209,668A
;  CURRENT FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-209-668-7

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 55;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 51
US-09-287-796-31/c
; Sequence 31, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0350
;  CURRENT APPLICATION NUMBER: US/09/287,796A
;  CURRENT FILING DATE: 1999-04-07
;  EARLIER APPLICATION NUMBER: 09/130,616
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-287-796-31

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 55;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 52
US-09-287-796-42
; Sequence 42, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0350
;  CURRENT APPLICATION NUMBER: US/09/287,796A
;  CURRENT FILING DATE: 1999-04-07
;  EARLIER APPLICATION NUMBER: 09/130,616
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-287-796-42

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 55;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db          7 GGCCTGGCCCGGAC 20


RESULT 53
US-09-130-616-31/c
; Sequence 31, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0318
;  CURRENT APPLICATION NUMBER: US/09/130,616C
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 31
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-130-616-31

  Query Match           38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 55;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 54
US-09-130-616-42
; Sequence 42, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0318
;  CURRENT APPLICATION NUMBER: US/09/130,616C
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-130-616-42

  Query Match           38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity  71.4%;  Pred. No. 55;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db          7 GGCCTGGCCCGGAC 20


RESULT 55
US-08-105-483-423
; Sequence 423, Application US/08105483
; Patent No. 5494807
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/105,483
;      FILING DATE:  12-AUG-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  423:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-105-483-423

  Query Match           35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAA 17
              |||||||
Db          1 GGCCAAA 7


RESULT 56
US-08-709-209-423
; Sequence 423, Application US/08709209
; Patent No. 5762938
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,209
;      FILING DATE:  21-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  423:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
```

```
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-709-209-423

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAA 17
               |||||||
Db          1 GGCCAAA 7


RESULT 57
US-08-303-275-131
; Sequence 131, Application US/08303275
; Patent No. 5766598
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS RECOMBINANT
;    TITLE OF INVENTION:  POXVIRUS VACCINE
;    NUMBER OF SEQUENCES:  205
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,275
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/897,382
;      FILING DATE:  11-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-303-275-131

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAA 17
               |||||||
Db          1 GGCCAAA 7


RESULT 58
US-08-458-101-423
; Sequence 423, Application US/08458101
; Patent No. 5766599
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Perkus, Marion E.
;    APPLICANT:  Taylor, Jill
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  No. 5766599ton, Elizabeth K.
;    APPLICANT:  Riviere, Michel
;    APPLICANT:  de Taisne, Charles
;    APPLICANT:  Limbach, Keith J.
;    APPLICANT:  Johnson, Gerard P.
;    APPLICANT:  Pincus, Steven E.
;    APPLICANT:  Cox, William I.
;    APPLICANT:  Audonnet, Jean-Christophe Francis
;    APPLICANT:  Gettig, Russell Robert
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  467
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,101
;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2740
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  423:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-458-101-423

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAAA 17
               |||||||
Db          1 GGCCAAA 7


RESULT 59
US-08-859-954-106
; Sequence 106, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
```

```
;       COUNTRY:  U.S.A.
;       ZIP:  77010-3095
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,954
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,782
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Paul, Thomas D.
;       REGISTRATION NUMBER:  32,714
;       REFERENCE/DOCKET NUMBER:  D-5900
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713/651-5325
;       TELEFAX:  713/651-5246
;   INFORMATION FOR SEQ ID NO:  106:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  YES
US-08-859-954-106

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
               |||||||
Db          1 GCCAAAG 7


RESULT 60
US-08-859-954-359
; Sequence 359, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  359:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-359

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CCAAAGT 19
               |||||||
Db          2 CCAAAGT 8


RESULT 61
US-08-474-700B-43/c
; Sequence 43, Application US/08474700B
; Patent No. 6001990
;  GENERAL INFORMATION:
;    APPLICANT:  Wands, Jack
;    APPLICANT:  Wakita, Takaji
;    APPLICANT:  Moradpour, Darius
;    TITLE OF INVENTION:  ANTISENSE INHIBITION OF HEPATITIS C
;    TITLE OF INVENTION:  VIRUS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,700B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,382
;      FILING DATE:  10 May 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/279001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-474-700B-43
```

```
  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||| ||
Db          8 GCCAGCCC 1


RESULT 62
US-08-859-954-56
; Sequence 56, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-56

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 GCCAAAGT 19
              | ||||||
Db          1 GGCAAAGT 8


RESULT 63
US-08-859-954-107
; Sequence 107, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  107:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-107

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 GCCAAAGT 19
              |||||| |
Db          1 GCCAAACT 8


RESULT 64
US-09-041-675-9/c
; Sequence 9, Application US/09041675A
; Patent No. 6100032
; GENERAL INFORMATION:
;  APPLICANT: Kern, Scott
;  APPLICANT: Zawel, Leigh
;  APPLICANT: Dai, Jia Le
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: Human SMAD3 and SMAD4 are
;  TITLE OF INVENTION: sequence-specific transcription activators
;  FILE REFERENCE: 01107.74098
;  CURRENT APPLICATION NUMBER: US/09/041,675A
;  CURRENT FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: synthetic random oligonucleotides selected for
;   OTHER INFORMATION: binding to human SMAD3 or human SMAD4
US-09-041-675-9

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              |||||| |
Db          8 GGCCAGAC 1


RESULT 65
US-09-041-675-15
; Sequence 15, Application US/09041675A
; Patent No. 6100032
; GENERAL INFORMATION:
;  APPLICANT: Kern, Scott
;  APPLICANT: Zawel, Leigh
;  APPLICANT: Dai, Jia Le
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: Human SMAD3 and SMAD4 are
;  TITLE OF INVENTION: sequence-specific transcription activators
;  FILE REFERENCE: 01107.74098
;  CURRENT APPLICATION NUMBER: US/09/041,675A
;  CURRENT FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic random oligonucleotides selected for
;   OTHER INFORMATION: binding to human SMAD3 or human SMAD4
US-09-041-675-15

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGC 8
              ||| ||||
Db          1 GTCTGGGC 8


RESULT 66
US-09-041-675-23
; Sequence 23, Application US/09041675A
; Patent No. 6100032
; GENERAL INFORMATION:
;  APPLICANT: Kern, Scott
;  APPLICANT: Zawel, Leigh
;  APPLICANT: Dai, Jia Le
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: Human SMAD3 and SMAD4 are
;  TITLE OF INVENTION: sequence-specific transcription activators
;  FILE REFERENCE: 01107.74098
;  CURRENT APPLICATION NUMBER: US/09/041,675A
;  CURRENT FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic random oligonucleotides selected for
;   OTHER INFORMATION: binding to human SMAD3 or human SMAD4
US-09-041-675-23

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGC 8
              ||| ||||
Db          1 GTCTGGGC 8


RESULT 67
US-08-646-301A-10
; Sequence 10, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
;  APPLICANT:  Richards, Cynthia Ann
;  APPLICANT:  Huber, Brian E.
;  TITLE OF INVENTION:  Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
;  TITLE OF INVENTION:  Antigen for Expression Targeting
;  FILE REFERENCE:  PB1508USW
;  CURRENT APPLICATION NUMBER: US/08/646,301A
;  CURRENT FILING DATE:  1996-05-16
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  consensus
;   OTHER INFORMATION: sequence B4  from DNA Sequence 1:3-11 (1990).
; Patent No. 6194211
US-08-646-301A-10

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              |:::|:||
Db          1 GSSWGSCC 8


RESULT 68
US-08-646-301A-10/c
; Sequence 10, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
;  APPLICANT:  Richards, Cynthia Ann
;  APPLICANT:  Huber, Brian E.
;  TITLE OF INVENTION:  Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
;  TITLE OF INVENTION:  Antigen for Expression Targeting
;  FILE REFERENCE:  PB1508USW
;  CURRENT APPLICATION NUMBER: US/08/646,301A
;  CURRENT FILING DATE:  1996-05-16
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  consensus
;   OTHER INFORMATION: sequence B4  from DNA Sequence 1:3-11 (1990).
; Patent No. 6194211
US-08-646-301A-10

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          6 GGCCAGGC 13
              ||:|:::|
Db          8 GGSCWSSC 1


RESULT 69
US-09-398-499-16/c
; Sequence 16, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
;  APPLICANT:  Benson, Andrew K.
;  TITLE OF INVENTION:  HIGH RESOLUTION GENOME SCANNING
;  FILE REFERENCE:  UNL 2963
;  CURRENT APPLICATION NUMBER: US/09/398,499
;  CURRENT FILING DATE:  1999-09-17
;  PRIOR APPLICATION NUMBER:. 60/101,011
;  PRIOR FILING DATE:  1998-09-18
;  NUMBER OF SEQ ID NOS:  58
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-16

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAG 11
              || |||||
Db          8 CGCGCCAG 1


RESULT 70
US-09-398-499-39
; Sequence 39, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
;  APPLICANT:  Benson, Andrew K.
;  TITLE OF INVENTION:  HIGH RESOLUTION GENOME SCANNING
;  FILE REFERENCE:  UNL 2963
;  CURRENT APPLICATION NUMBER: US/09/398,499
;  CURRENT FILING DATE:  1999-09-17
;  PRIOR APPLICATION NUMBER:  60/101,011
;  PRIOR FILING DATE:  1998-09-18
;  NUMBER OF SEQ ID NOS:  58
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 39
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-39

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAG 11
              || |||||
Db          1 CGCGCCAG 8


RESULT 71
US-08-522-384-63
; Sequence 63, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
;  APPLICANT: LOPEZ-NIETO, CARLOS E
;  APPLICANT: NIGAM, SANJAY KUMAR
;  TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
;  TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 2458-4029
;  CURRENT APPLICATION NUMBER: US/08/522,384
;  CURRENT FILING DATE: 1996-11-15
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:  Primer
US-08-522-384-63

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 54;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||| ||||
Db          1 GCCTGGCC 8


RESULT 72
US-08-584-040-7661
; Sequence 7661, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7661:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
```

```
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-584-040-7661

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 66;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              |||| |||
Db         10 GGCCUGGC 17


RESULT 73
US-09-371-772B-3450
; Sequence 3450, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3450
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-3450

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 66;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              |||| |||
Db         10 GGCCUGGC 17


RESULT 74
US-07-949-541A-34/c
; Sequence 34, Application US/07949541A
; Patent No. 5552270
;  GENERAL INFORMATION:
;    APPLICANT:  Khrapko, Konstantin R.
;    APPLICANT:  Khorlin, Alexandr A.
;    APPLICANT:  Ivanov, Igor B.
;    APPLICANT:  Ershov, Gennady M.
;    APPLICANT:  Lysov, Jury P.
;    APPLICANT:  Florentiev, Vladimir L.
;    APPLICANT:  Mirzabekov, Andrei D.
;    TITLE OF INVENTION:  Method for Determining a DNA Nucleotide
;    TITLE OF INVENTION:  Sequence and a Device for Carrying Out Same
; Patent No. 5552270
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ladas & Parry
;      STREET:  26 West 61st Street
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10023
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 Kb storage
;      COMPUTER:  IBM PC/XT/AT or compatibles
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/949,541A
;      FILING DATE:  09-No. 5552270-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/RU92/00052
;      FILING DATE:  18-Mar-1992
;      APPLICATION NUMBER:  Russian Federation 4919321
;      FILING DATE:  18-Mar-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janet I. Cord
;      REGISTRATION NUMBER:  33,778
;      REFERENCE/DOCKET NUMBER:  U-8999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 708-1800
;      TELEFAX:  (212) 246-8959
;      TELEX:  233288
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  chemically synthesized
;    MOLECULE TYPE:  desoxyribooligonucleotide.
;    FEATURE:  oligonucleotide was synthesized by phosphoroamidite
;    FEATURE:  method.
;      OTHER INFORMATION:  letter M means the tethering to the
;      OTHER INFORMATION:  support via oxidized 3-methyluridine.
US-07-949-541A-34

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAG 11
              ||||||
Db          6 GGCCAG 1


RESULT 75
US-07-949-541A-39/c
; Sequence 39, Application US/07949541A
; Patent No. 5552270
;  GENERAL INFORMATION:
;    APPLICANT:  Khrapko, Konstantin R.
;    APPLICANT:  Khorlin, Alexandr A.
;    APPLICANT:  Ivanov, Igor B.
;    APPLICANT:  Ershov, Gennady M.
;    APPLICANT:  Lysov, Jury P.
;    APPLICANT:  Florentiev, Vladimir L.
;    APPLICANT:  Mirzabekov, Andrei D.
;    TITLE OF INVENTION:  Method for Determining a DNA Nucleotide
;    TITLE OF INVENTION:  Sequence and a Device for Carrying Out Same
; Patent No. 5552270
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ladas & Parry
;      STREET:  26 West 61st Street
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10023
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 Kb storage
;      COMPUTER:  IBM PC/XT/AT or compatibles
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/07/949,541A
;      FILING DATE:  09-No. 5552270-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/RU92/00052
;      FILING DATE:  18-Mar-1992
;      APPLICATION NUMBER:  Russian Federation 4919321
;      FILING DATE:  18-Mar-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janet I. Cord
;      REGISTRATION NUMBER:  33,778
;      REFERENCE/DOCKET NUMBER:  U-8999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 708-1800
;      TELEFAX:  (212) 246-8959
;      TELEX:  233288
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  chemically synthesized
;    MOLECULE TYPE:  desoxyribooligonucleotide.
;    FEATURE:  oligonucleotide was synthesized by phosphoroamidite
;    FEATURE:  method.
;      OTHER INFORMATION:  letter M means the tethering to the
;      OTHER INFORMATION:  support via oxidized 3-methyluridine.
US-07-949-541A-39

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAG 11
              ||||||
Db          7 GGCCAG 2


RESULT 76
US-08-593-345B-13/c
; Sequence 13, Application US/08593345B
; Patent No. 5851772
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Lysov, Yuriy P
;    APPLICANT:  Shick, Valentine V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  A Microchip Method for the Enrichment of
;    TITLE OF INVENTION:  Specific DNA Sequences.
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/593,345B
;      FILING DATE:  29-JAN-96
;    PRIOR APPLICATION DATA:  No. 5851772e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-029+30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 5851772 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    FEATURE:
;      NAME/KEY:  No. 5851772e
;      LOCATION:  1-8
;      IDENTIFICATION METHOD:  Similarity with known sequences.
;      OTHER INFORMATION:  Complementarity with primer of
;      OTHER INFORMATION:  exons to a-thalassemia gene.
US-08-593-345B-13

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAA 16
              ||||||
Db          8 GGCCAA 3


RESULT 77
US-08-859-954-53/c
; Sequence 53, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-53
```

```
  Query Match           30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 AAAGTC 20
               ||||||
Db          8 AAAGTC 3


RESULT 78
US-08-859-954-81/c
; Sequence 81, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  81:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-81

  Query Match           30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CCAAAG 18
               ||||||
Db          7 CCAAAG 2


RESULT 79
US-08-859-954-104
; Sequence 104, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  104:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-104

  Query Match           30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAA 17
               ||||||
Db          1 GCCAAA 6


RESULT 80
US-08-859-954-329/c
; Sequence 329, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  329:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-329

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 AAAGTC 20
              ||||||
Db          8 AAAGTC 3


RESULT 81
US-08-859-954-332
; Sequence 332, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  332:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-332

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 CAAAGT 19
              ||||||
Db          3 CAAAGT 8


RESULT 82
US-08-859-954-333/c
; Sequence 333, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  333:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-333

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
```

```
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CCAAAG 18
              ||||||
Db          7 CCAAAG 2


RESULT 83
US-08-859-954-360
; Sequence 360, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  360:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "olgionucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-360

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CCAAAG 18
              ||||||
Db          2 CCAAAG 7


RESULT 84
US-08-859-954-396
; Sequence 396, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  396:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-396

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GGCCAA 16
              ||||||
Db          3 GGCCAA 8


Search completed: November 10, 2003, 08:03:59
Job time : 1 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 08:06:57 ; Search time 0.001 Seconds
(without alignments)
27.440 Million cell updates/sec

Title: us-09-774-809-31
Perfect score: 20
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 63 seqs, 686 residues

Total number of hits satisfying chosen parameters: 126

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 86 summaries

Database : rnpb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	US-09-774-809-31	Sequence 31, Appl
c	2	20	100.0	20	1	US-09-774-809-42	Sequence 42, Appl
	3	20	100.0	20	1	US-09-888-326-463	Sequence 463, App
	4	20	100.0	20	1	US-09-776-479-311	Sequence 311, App
	5	20	100.0	20	1	US-10-112-653-301	Sequence 301, App
	6	20	100.0	20	1	US-10-017-995-311	Sequence 311, App
	7	17	85.0	20	1	US-10-007-010-56	Sequence 56, Appl
	8	13.4	67.0	17	1	US-10-020-038-6	Sequence 6, Appli
c	9	10	50.0	10	1	US-10-330-627-1410	Sequence 1410, Ap
c	10	10	50.0	10	1	US-10-330-627-1411	Sequence 1411, Ap
	11	10	50.0	12	1	US-09-263-959-437	Sequence 437, App
	12	9.8	49.0	13	1	US-10-005-212-7	Sequence 7, Appli
c	13	9	45.0	10	1	US-10-033-145-1619	Sequence 1619, Ap
c	14	9	45.0	11	1	US-10-055-728-15	Sequence 15, Appl
c	15	8.8	44.0	12	1	US-09-263-959-437	Sequence 437, App
c	16	8.6	43.0	20	1	US-10-007-010-56	Sequence 56, Appl
c	17	8.4	42.0	10	1	US-10-329-465-204	Sequence 204, App
c	18	8.4	42.0	10	1	US-10-330-627-420	Sequence 420, App
c	19	8.4	42.0	10	1	US-10-330-627-421	Sequence 421, App
	20	8.4	42.0	10	1	US-10-330-627-422	Sequence 422, App
	21	8.4	42.0	10	1	US-10-330-627-644	Sequence 644, App
c	22	8.4	42.0	10	1	US-10-330-627-1228	Sequence 1228, Ap
c	23	8.4	42.0	10	1	US-10-330-627-1229	Sequence 1229, Ap
c	24	8.4	42.0	10	1	US-10-330-627-1230	Sequence 1230, Ap
c	25	8.4	42.0	10	1	US-10-330-627-1231	Sequence 1231, Ap
c	26	8.4	42.0	10	1	US-10-330-627-1232	Sequence 1232, Ap
c	27	8.4	42.0	10	1	US-10-330-627-1233	Sequence 1233, Ap
c	28	8.4	42.0	10	1	US-10-330-627-1234	Sequence 1234, Ap
c	29	8.4	42.0	10	1	US-10-033-145-405	Sequence 405, App
	30	8.4	42.0	10	1	US-10-033-145-1326	Sequence 1326, Ap
	31	8.4	42.0	11	1	US-10-055-728-4	Sequence 4, Appli
c	32	8	40.0	9	1	US-09-989-789-2374	Sequence 2374, Ap
c	33	8	40.0	9	1	US-09-989-789-2376	Sequence 2376, Ap
c	34	8	40.0	9	1	US-09-989-789-2424	Sequence 2424, Ap
c	35	8	40.0	9	1	US-09-990-186-2374	Sequence 2374, Ap
c	36	8	40.0	9	1	US-09-990-186-2376	Sequence 2376, Ap
c	37	8	40.0	9	1	US-09-990-186-2424	Sequence 2424, Ap
c	38	8	40.0	9	1	US-09-989-994-2374	Sequence 2374, Ap
c	39	8	40.0	9	1	US-09-989-994-2376	Sequence 2376, Ap
c	40	8	40.0	9	1	US-09-989-994-2424	Sequence 2424, Ap
	41	8	40.0	10	1	US-10-330-627-1228	Sequence 1228, Ap
	42	8	40.0	10	1	US-10-330-627-1229	Sequence 1229, Ap
	43	8	40.0	10	1	US-10-330-627-1230	Sequence 1230, Ap
	44	8	40.0	10	1	US-10-330-627-1231	Sequence 1231, Ap
	45	8	40.0	10	1	US-10-330-627-1232	Sequence 1232, Ap
	46	8	40.0	10	1	US-10-330-627-1233	Sequence 1233, Ap
	47	8	40.0	10	1	US-10-330-627-1234	Sequence 1234, Ap
	48	8	40.0	10	1	US-10-330-627-621	Sequence 621, App
c	49	8	40.0	10	1	US-10-330-627-876	Sequence 876, App
c	50	8	40.0	10	1	US-10-330-627-877	Sequence 877, App
c	51	8	40.0	10	1	US-10-330-627-1214	Sequence 1214, Ap
c	52	8	40.0	10	1	US-10-330-627-1215	Sequence 1215, Ap
c	53	8	40.0	10	1	US-10-438-683-6	Sequence 6, Appli
c	54	8	40.0	10	1	US-10-033-145-62	Sequence 62, Appl
c	55	8	40.0	10	1	US-10-033-145-1531	Sequence 1531, Ap
c	56	8	40.0	10	1	US-10-033-145-1750	Sequence 1750, Ap
	57	7.8	39.0	11	1	US-10-055-728-15	Sequence 15, Appl
c	58	7.8	39.0	17	1	US-10-020-038-6	Sequence 6, Appli
c	59	7.6	38.0	20	1	US-09-774-809-31	Sequence 31, Appl
	60	7.6	38.0	20	1	US-09-774-809-42	Sequence 42, Appl
c	61	7.6	38.0	20	1	US-09-888-326-463	Sequence 463, App
c	62	7.6	38.0	20	1	US-09-776-479-311	Sequence 311, App
c	63	7.6	38.0	20	1	US-10-112-653-301	Sequence 301, App
c	64	7.6	38.0	20	1	US-10-017-995-311	Sequence 311, App
	65	7.4	37.0	9	1	US-09-989-789-2148	Sequence 2148, Ap
	66	7.4	37.0	9	1	US-09-989-789-2149	Sequence 2149, Ap
	67	7.4	37.0	9	1	US-09-990-186-2148	Sequence 2148, Ap
	68	7.4	37.0	9	1	US-09-990-186-2149	Sequence 2149, Ap
	69	7.4	37.0	9	1	US-09-989-994-2148	Sequence 2148, Ap
	70	7.4	37.0	9	1	US-09-989-994-2149	Sequence 2149, Ap
	71	7.4	37.0	9	1	US-10-277-494-167	Sequence 167, App
	72	7.4	37.0	10	1	US-10-033-145-405	Sequence 405, App
	73	7.4	37.0	10	1	US-10-330-627-1214	Sequence 1214, Ap
	74	7.4	37.0	10	1	US-10-330-627-1215	Sequence 1215, Ap
c	75	7	35.0	8	1	US-09-837-751-13	Sequence 13, Appl
c	76	7	35.0	9	1	US-09-989-789-2396	Sequence 2396, Ap
c	77	7	35.0	9	1	US-09-989-789-2397	Sequence 2397, Ap
c	78	7	35.0	9	1	US-09-990-186-2396	Sequence 2396, Ap
c	79	7	35.0	9	1	US-09-990-186-2397	Sequence 2397, Ap
c	80	7	35.0	9	1	US-09-989-994-2396	Sequence 2396, Ap
c	81	7	35.0	9	1	US-09-989-994-2397	Sequence 2397, Ap
	82	6.8	34.0	10	1	US-10-330-627-876	Sequence 876, App
	83	6.8	34.0	10	1	US-10-330-627-877	Sequence 877, App
	84	6.8	34.0	10	1	US-10-033-145-1750	Sequence 1750, Ap
	85	6.4	32.0	8	1	US-10-027-632-176277	Sequence 176277,
	86	6.4	32.0	8	1	US-10-027-632-176277	Sequence 176277,

ALIGNMENTS

RESULT 1
US-09-774-809-31
; Sequence 31, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0412
; CURRENT APPLICATION NUMBER: US/09/774,809
; CURRENT FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 09/396,902
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/130,616
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 08/910,629
; PRIOR FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-774-809-31

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCCAAAGTC 20
||||||||||||||||||||
Db 1 GTCCGGGCCAGGCCAAAGTC 20

RESULT 2
US-09-774-809-42/c
; Sequence 42, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0412
; CURRENT APPLICATION NUMBER: US/09/774,809
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/396,902
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/130,616
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 08/910,629
; PRIOR FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-774-809-42

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCCAAAGTC 20
||||||||||||||||||||
Db 20 GTCCGGGCCAGGCCAAAGTC 1

RESULT 3
US-09-888-326-463
; Sequence 463, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-463

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCCAAAGTC 20
||||||||||||||||||||
Db 1 GTCCGGGCCAGGCCAAAGTC 20

RESULT 4
US-09-776-479-311
; Sequence 311, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-311

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGGGCCAGGCCAAAGTC 20
||||||||||||||||||||
Db 1 GTCCGGGCCAGGCCAAAGTC 20

RESULT 5
US-10-112-653-301
; Sequence 301, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642

```
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 301
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-301

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.076;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 6
US-10-017-995-311
; Sequence 311, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-311

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.076;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCCAAAGTC 20
              ||||||||||||||||||||
Db          1 GTCCGGGCCAGGCCAAAGTC 20


RESULT 7
US-10-007-010-56
; Sequence 56, Application US/10007010
; Publication No. US20030125275A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander H. Borchers
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
;  FILE REFERENCE: RTS-0345
;  CURRENT APPLICATION NUMBER: US/10/007,010
;  CURRENT FILING DATE:  2001-12-04
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-010-56

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.59;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCAAAGT 19
              |||||||||||||||||
Db          4 CCGGGCCAGGCCAAAGT 20


RESULT 8
US-10-020-038-6
; Sequence 6, Application US/10020038
; Publication No. US20020156247A1
; GENERAL INFORMATION:
;  APPLICANT: Elledge, Stephen J.
;  APPLICANT:  Sanchez, Yolanda
;  TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
;  FILE REFERENCE: 120541-1013
;  CURRENT APPLICATION NUMBER: US/10/020,038
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: US/09/488,364
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-10-020-038-6

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 3.8;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              || ||||||||||||
Db          3 GGACAGGCCAAAGTC 17


RESULT 9
US-10-330-627-1410/c
; Sequence 1410, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1410
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1410

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||||||||||
Db         10 TCCGGGCCAG 1


RESULT 10
US-10-330-627-1411/c
; Sequence 1411, Application US/10330627
```

```
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1411
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1411

  Query Match             50.0%; Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCCGGGCCAG 11
              ||||||||||
Db         10 TCCGGGCCAG 1


RESULT 11
US-09-263-959-437
; Sequence 437, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  437:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-437

  Query Match             50.0%;  Score 10;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              ||||||||||
Db          1 GGCCAGGCCA 10


RESULT 12
US-10-005-212-7
; Sequence 7, Application US/10005212
; Publication No. US20020193570A1
; GENERAL INFORMATION:
;  APPLICANT: GILLIES, Stephen D
;  APPLICANT:  LAN, Yan
;  APPLICANT:  LO, Kin-Ming
;  TITLE OF INVENTION: Heterodimeric Fusion Proteins Useful for Targeted
;  TITLE OF INVENTION:  Immune Therapy and General Immune Stimulation
;  FILE REFERENCE: LEX-002C1
;  CURRENT APPLICATION NUMBER: US/10/005,212
;  CURRENT FILING DATE:  2001-12-04
;  PRIOR APPLICATION NUMBER: USSN 08/986,997
;  PRIOR FILING DATE: 1997-12-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Oligonucleotide
US-10-005-212-7

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 16;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCCA 15
              |||||| || |||
Db          1 CCGGGCAAGTCCA 13


RESULT 13
US-10-033-145-1619/c
; Sequence 1619, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1619
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1619

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAG 18
              |||||||||
Db         10 AGGCCAAAG 2


RESULT 14
US-10-055-728-15/c
```

```
; Sequence 15, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
;  APPLICANT: van der Kuyl, Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
;  FILE REFERENCE: 5244US (REN/P55190US00)
;  CURRENT APPLICATION NUMBER: US/10/055,728
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 0120373.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: TAG sequence Hs74649
US-10-055-728-15

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCC 14
              |||||||||
Db         11 GGCCAGGCC 3


RESULT 15
US-09-263-959-437/c
; Sequence 437, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  437:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-437

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 23;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAGGCC 14
              || |||| ||||
Db         12 CCTGGCCTGGCC 1


RESULT 16
US-10-007-010-56/c
; Sequence 56, Application US/10007010
; Publication No. US20030125275A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander H. Borchers
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
;  FILE REFERENCE: RTS-0345
;  CURRENT APPLICATION NUMBER: US/10/007,010
;  CURRENT FILING DATE:  2001-12-04
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-010-56

  Query Match             43.0%;  Score 8.6;  DB 1;  Length 20;
  Best Local Similarity   73.3%;  Pred. No. 46;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAAAGTC 20
              |||| ||||   |||
Db         15 GGCCTGGCCCGGGTC 1


RESULT 17
US-10-329-465-204/c
; Sequence 204, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
;  APPLICANT: Wang et al.
;  TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-A
;  TITLE OF INVENTION:  FUSION
;  FILE REFERENCE: 27373/37928A
;  CURRENT APPLICATION NUMBER: US/10/329,465
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: US 60/343,826
;  PRIOR FILING DATE: 2001-12-27
;  NUMBER OF SEQ ID NOS: 315
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-204

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGCC 14
              | ||||||||
Db         10 GTGCCAGGCC 1


RESULT 18
```

```
US-10-330-627-420/c
; Sequence 420, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 420
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-420

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 19
US-10-330-627-421/c
; Sequence 421, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 421
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-421

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCA 15
              || |||||||
Db         10 GGGCAGGCCA 1


RESULT 20
US-10-330-627-422
; Sequence 422, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 422
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-422

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              ||||||| |
Db          1 GGCCAAAGGC 10


RESULT 21
US-10-330-627-644
; Sequence 644, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 644
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-644

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10


RESULT 22
US-10-330-627-1228/c
; Sequence 1228, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1228
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1228

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
```

```
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 23
US-10-330-627-1229/c
; Sequence 1229, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1229
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1229

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 24
US-10-330-627-1230/c
; Sequence 1230, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1230
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1230

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 25
US-10-330-627-1231/c
; Sequence 1231, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1231
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1231

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 26
US-10-330-627-1232/c
; Sequence 1232, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1232
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1232

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 27
US-10-330-627-1233/c
; Sequence 1233, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
```

```
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1233
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1233

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 28
US-10-330-627-1234/c
; Sequence 1234, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1234
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1234

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||| ||||||
Db         10 GCCTGGCCAA 1


RESULT 29
US-10-033-145-405/c
; Sequence 405, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 405
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-405

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCCAA 16
              ||||||||| |
Db         10 GCCAGGCCCA 1


RESULT 30
US-10-033-145-1326
; Sequence 1326, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1326
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1326

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGCCAAAGT 19
              || |||||||
Db          1 AGACCAAAGT 10


RESULT 31
US-10-055-728-4
; Sequence 4, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
;  APPLICANT: van der Kuyl, Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
;  FILE REFERENCE: 5244US (REN/P55190US00)
;  CURRENT APPLICATION NUMBER: US/10/055,728
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 0120373.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: TAG sequence Hs78436
US-10-055-728-4

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 23;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GGCCAAAGTC 20
              |||||||| |
Db          1 GGCCAAAGGC 10
```

```
RESULT 32
US-09-989-789-2374/c
; Sequence 2374, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2374
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2374

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 33
US-09-989-789-2376/c
; Sequence 2376, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2376
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2376

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 34
US-09-989-789-2424/c
; Sequence 2424, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2424
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2424

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 35
US-09-990-186-2374/c
; Sequence 2374, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2374
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2374

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 36
US-09-990-186-2376/c
; Sequence 2376, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2376
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2376
```

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 37
US-09-990-186-2424/c
; Sequence 2424, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2424
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2424

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 38
US-09-989-994-2374/c
; Sequence 2374, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2374
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2374

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 39
US-09-989-994-2376/c
; Sequence 2376, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2376
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2376

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 40
US-09-989-994-2424/c
; Sequence 2424, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2424
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2424

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              ||||||||
Db          9 CCAGGCCA 2


RESULT 41
US-10-330-627-1228
; Sequence 1228, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
```

```
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1228
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1228

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 42
US-10-330-627-1229
; Sequence 1229, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1229
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1229

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 43
US-10-330-627-1230
; Sequence 1230, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1230
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1230

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 44
US-10-330-627-1231
; Sequence 1231, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1231
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1231

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 45
US-10-330-627-1232
; Sequence 1232, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1232
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1232

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 46
US-10-330-627-1233
; Sequence 1233, Application US/10330627
; Publication No. US20030175771A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1233
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1233

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 47
US-10-330-627-1234
; Sequence 1234, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1234
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1234

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          3 GGCCAGGC 10


RESULT 48
US-10-330-627-621
; Sequence 621, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 621
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-621

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGG 12
              ||||||||
Db          1 GGGCCAGG 8


RESULT 49
US-10-330-627-876/c
; Sequence 876, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 876
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-876

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 50
US-10-330-627-877/c
; Sequence 877, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 877
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-877

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 51
US-10-330-627-1214/c
; Sequence 1214, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1214
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1214

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 52
US-10-330-627-1215/c
; Sequence 1215, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1215
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1215

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGC 13
              ||||||||
Db          8 GGCCAGGC 1


RESULT 53
US-10-438-683-6/c
; Sequence 6, Application US/10438683
; Publication No. US20030186923A1
;   GENERAL INFORMATION:
;        APPLICANT: JAMES D. THOMPSON
;        TITLE OF INVENTION: METHOD AND REAGENT FOR
;                            INHIBITING P-GLYCOPROTEIN mdr-
;                            1 GENE
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 611 West Sixth Street
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: USA
;             ZIP: 90017
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;             COMPUTER: IBM COMPATIBLE
;             OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;             SOFTWARE: WordPerfect (Version 5.1)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/438,683
;             FILING DATE: 15-May-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/07/882,885
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 197/173
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-438-683-6

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAGT 19
              ||||||||
Db         10 GCCAAAGT 3


RESULT 54
US-10-033-145-62/c
; Sequence 62, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-62

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGCCAA 16
              ||||||||
Db         10 CAGGCCAA 3


RESULT 55
US-10-033-145-1531/c
; Sequence 1531, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1531
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1531

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CCAAAGTC 20
              ||||||||
Db          8 CCAAAGTC 1


RESULT 56
US-10-033-145-1750/c
; Sequence 1750, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1750
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1750

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GCCAGGCC 14
              ||||||||
Db         10 GCCAGGCC 3


RESULT 57
US-10-055-728-15
; Sequence 15, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
;  APPLICANT: van der Kuyl, Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
;  FILE REFERENCE: 5244US (REN/P55190US00)
;  CURRENT APPLICATION NUMBER: US/10/055,728
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 0120373.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: TAG sequence Hs74649
US-10-055-728-15

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 32;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGCC 14
              | |||| ||||
Db          1 CAGGCCTGGCC 11


RESULT 58
US-10-020-038-6/c
; Sequence 6, Application US/10020038
; Publication No. US20020156247A1
; GENERAL INFORMATION:
;  APPLICANT: Elledge, Stephen J.
;  APPLICANT:  Sanchez, Yolanda
;  TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
;  FILE REFERENCE: 120541-1013
;  CURRENT APPLICATION NUMBER: US/10/020,038
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: US/09/488,364
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-10-020-038-6

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCCAGGCCAA 16
              |||| | ||||
Db         11 GGCCTGTCCAA 1


RESULT 59
US-09-774-809-31/c
; Sequence 31, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Monia, Brett
;  APPLICANT:  Nero, Pam
```

```
;  APPLICANT:  Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION:  FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0412
;  CURRENT APPLICATION NUMBER: US/09/774,809
;  CURRENT FILING DATE:  2001-01-31
;  PRIOR APPLICATION NUMBER: 09/396,902
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 09/130,616
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 08/910,629
;  PRIOR FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-774-809-31

  Query Match           38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 60
US-09-774-809-42
; Sequence 42, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Monia, Brett
;  APPLICANT:  Nero, Pam
;  APPLICANT:  Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION:  FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0412
;  CURRENT APPLICATION NUMBER: US/09/774,809
;  CURRENT FILING DATE:  2001-01-31
;  PRIOR APPLICATION NUMBER: 09/396,902
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 09/130,616
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 08/910,629
;  PRIOR FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-774-809-42

  Query Match           38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db          7 GGCCTGGCCCGGAC 20


RESULT 61
US-09-888-326-463/c
; Sequence 463, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 463
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-463

  Query Match           38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 62
US-09-776-479-311/c
; Sequence 311, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-311

  Query Match           38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 63
US-10-112-653-301/c
; Sequence 301, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
```

```
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 301
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-301

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 64
US-10-017-995-311/c
; Sequence 311, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-311

  Query Match             38.0%;  Score 7.6;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GTCCGGGCCAGGCC 14
              | || |||| || |
Db         14 GGCCTGGCCCGGAC 1


RESULT 65
US-09-989-789-2148
; Sequence 2148, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2148
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2148

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 66
US-09-989-789-2149
; Sequence 2149, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2149
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2149

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 67
US-09-990-186-2148
; Sequence 2148, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2148
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2148

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
```

```
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 68
US-09-990-186-2149
; Sequence 2149, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2149
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2149

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 69
US-09-989-994-2148
; Sequence 2148, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2148
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2148

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 70
US-09-989-994-2149
; Sequence 2149, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2149
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2149

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GGGCCAGGC 13
              ||| |||||
Db          1 GGGGCAGGC 9


RESULT 71
US-10-277-494-167
; Sequence 167, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Levels
;  TITLE OF INVENTION:  Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-K (400/064)
;  CURRENT APPLICATION NUMBER: US/10/277,494
;  CURRENT FILING DATE:  2002-10-21
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
;   LENGTH: 9
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-277-494-167

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CCGGGCCAG 11
              | |||||||
Db          1 CUGGGCCAG 9


RESULT 72
US-10-033-145-405
; Sequence 405, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 405
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

US-10-033-145-405

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCCAGGC 13
||||| |||
Db 2 GGGCCTGGC 10

RESULT 73
US-10-330-627-1214
; Sequence 1214, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1214
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1214

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCCAGGCCA 15
||| |||||
Db 1 GCCTGGCCA 9

RESULT 74
US-10-330-627-1215
; Sequence 1215, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1215
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1215

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCCAGGCCA 15
||| |||||
Db 1 GCCTGGCCA 9

RESULT 75
US-09-837-751-13/c
; Sequence 13, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: oligonucleotide useful as a primer
US-09-837-751-13

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCGGGCC 9
|||||||
Db 7 CCGGGCC 1

RESULT 76
US-09-989-789-2396/c
; Sequence 2396, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2396
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2396

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GCCAAAG 18
|||||||
Db 8 GCCAAAG 2

RESULT 77
US-09-989-789-2397/c
; Sequence 2397, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

```
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2397
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2397

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          8 GCCAAAG 2


RESULT 78
US-09-990-186-2396/c
; Sequence 2396, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2396
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2396

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          8 GCCAAAG 2


RESULT 79
US-09-990-186-2397/c
; Sequence 2397, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2397
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2397

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          8 GCCAAAG 2


RESULT 80
US-09-989-994-2396/c
; Sequence 2396, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2396
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2396

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          8 GCCAAAG 2


RESULT 81
US-09-989-994-2397/c
; Sequence 2397, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2397
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2397

  Query Match            35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GCCAAAG 18
              |||||||
Db          8 GCCAAAG 2
```

```
RESULT 82
US-10-330-627-876
; Sequence 876, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 876
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-876

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 42;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||  |||
Db          1 CAGGCCTGGC 10


RESULT 83
US-10-330-627-877
; Sequence 877, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 877
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-877

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 42;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||  |||
Db          1 CAGGCCTGGC 10


RESULT 84
US-10-033-145-1750
; Sequence 1750, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1750
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1750

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 42;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CGGGCCAGGC 13
              | ||||  |||
Db          1 CAGGCCTGGC 10


RESULT 85
US-10-027-632-176277
; Sequence 176277, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 176277
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-176277

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              |||| |||
Db          1 CCAGCCCA 8


RESULT 86
US-10-027-632-176277
; Sequence 176277, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
```

```
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 176277
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-176277

  Query Match            32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity  87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CCAGGCCA 15
              |||| |||
Db          1 CCAGCCCA 8


Search completed: November 10, 2003, 08:06:57
Job time : 0.001 secs
```

THIS PAGE BLANK (USPTO)

OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 08:08:11 ; Search time 0.001 Seconds
(without alignments)
0.320 Million cell updates/sec

Title: us-09-774-809-31
Perfect score: 20
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 8 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : rst.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	6	30.0	8	1	CD486474	ACCESSION:CD486474
	2	2.4	12.0	8	1	CD486474	ACCESSION:CD486474

ALIGNMENTS

RESULT 1
CD486474/c
LOCUS CD486474 8 bp mRNA linear EST 04-JUN-2003
DEFINITION CRH2.4F08 Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)
Gossypium hirsutum cDNA clone CRH2.4F08 5', mRNA sequence.
ACCESSION CD486474
VERSION CD486474.1 GI:31407439
KEYWORDS EST.
SOURCE Gossypium hirsutum (upland cotton)
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 8)
AUTHORS Dowd,C., Wilson,I. and McFadden,H.
TITLE Different Gene Expression Responses in Cotton Root and Hypocotyl tissues during infection with Fusarium Wilt Disease
JOURNAL Unpublished (2003)
COMMENT Contact: Caitriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive,
Black Mountain, Canberra, ACT, 2601, Australia
Tel: 61 2 6246 4914, 6246 5377
Fax: 61 2 6246 5000
Email: Caitriona.Dowd@csiro.au, Helen.McFadden@csiro.au
Vector clipped sequences Bases 1-17 (GTCGACCCACGCGTCCG): SalI adapter
Seq primer: M13 reverse primer
High quality sequence stop: 8.
FEATURES Location/Qualifiers
source 1. .8
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="DeltaEMERALD"
/db_xref="taxon:3635"
/clone="CRH2.4F08"
/tissue_type="Root and hypocotyl tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
/clone_lib="Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)"
/note="Vector: Lambda ZIPLOX; Site_1: SalI; Site_2: NotI; mRNA was prepared from root and hypocotyl tissues of the cotton cultivar DeltaEMERALD. cDNA was synthesised from a NotI-oligodT primer/adapter using the manufacturers protocols (Life Technologies) and then ligated to a SalI adapter to facilitate directional cloning. The cDNA was cloned into the SalI and NotI sites of the Lambda ZIPLOX phage vector (Life Technologies). Constructed by Caitriona Dowd and Helen McFadden."
BASE COUNT 3 a 1 c 1 g 3 t

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CAAAGT 19
||||||
Db 7 CAAAGT 2

RESULT 2
CD486474
LOCUS CD486474 8 bp mRNA linear EST 04-JUN-2003
DEFINITION CRH2.4F08 Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)
Gossypium hirsutum cDNA clone CRH2.4F08 5', mRNA sequence.
ACCESSION CD486474
VERSION CD486474.1 GI:31407439
KEYWORDS EST.
SOURCE Gossypium hirsutum (upland cotton)
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 8)
AUTHORS Dowd,C., Wilson,I. and McFadden,H.
TITLE Different Gene Expression Responses in Cotton Root and Hypocotyl tissues during infection with Fusarium Wilt Disease
JOURNAL Unpublished (2003)
COMMENT Contact: Caitriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive,
Black Mountain, Canberra, ACT, 2601, Australia
Tel: 61 2 6246 4914, 6246 5377
Fax: 61 2 6246 5000
Email: Caitriona.Dowd@csiro.au, Helen.McFadden@csiro.au
Vector clipped sequences Bases 1-17 (GTCGACCCACGCGTCCG): SalI adapter
Seq primer: M13 reverse primer
High quality sequence stop: 8.
FEATURES Location/Qualifiers
source 1. .8
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="DeltaEMERALD"
/db_xref="taxon:3635"
/clone="CRH2.4F08"

/tissue_type="Root and hypocotyl tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
/clone_lib="Cotton Root and Hypocotyl Lambda ZIPLOX
Library (CRH)"
/note="Vector: Lambda ZIPLOX; Site_1: SalI; Site_2: NotI;
mRNA was prepared from root and hypocotyl tissues of the
cotton cultivar DeltaEMERALD. cDNA was synthesised from a
NotI-oligodT primer/adapter using the manufacturers
protocols (Life Technologies) and then ligated to a SalI
adapter to facilitate directional cloning. The cDNA was
cloned into the SalI and NotI sites of the Lambda ZIPLOX
phage vector (Life Technologies). Constructed by Caitriona
Dowd and Helen McFadden."

BASE COUNT 3 a 1 c 1 g 3 t

Query Match 12.0%; Score 2.4; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          16 AAGT 19
               || |
Db           1 AACT 4
```

Search completed: November 10, 2003, 08:08:11
Job time : 0.001 secs